

STIC-Biotech/ChemLib

125072

**From:** Page, Thurman  
**Sent:** Friday, June 18, 2004 2:31 PM  
**To:** STIC-Biotech/ChemLib  
**Cc:** Basi, Nirmal; Page, Thurman  
**Subject:** FW: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

TWO MONTH AMENDMENT: RUSH SEARCH APPROVED

Thurman K. Page  
SPE Art Units 1615 & 1616  
Technology Center 1600

-----Original Message-----

**From:** Basi, Nirmal  
**Sent:** Friday, June 18, 2004 1:21 PM  
**To:** Page, Thurman  
**Subject:** FW: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

Thurman, Cristina is out of the office, could you approve a rush search please.

-----Original Message-----

**From:** Basi, Nirmal  
**Sent:** Friday, June 18, 2004 1:18 PM  
**To:** Chan, Christina  
**Subject:** Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

Christina I am seeking approval for a RUSH sequence search, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi  
Art Unit 1646  
Office: Remsen Building, Room 4D68  
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 09/429,832 (please use the sequence listing in parent application 08/906,365 to do the search)

Result format: Paper.

Title NOVEL HUMAN ESTROGEN RECEPTOR-BETA  
Inventors: BHAT, RAMESH A. et al

Priority Date: 8/5/97

Please search:

i) SEQ ID NO:2

RECEIVED  
JUN 18 2004  
STIC

Searcher: Jan  
Phone: 72504  
Location: \_\_\_\_\_  
Date Picked Up: 6/20  
Date Completed: 6/20  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: 10  
Online time: 10

TYPE OF SEARCH:

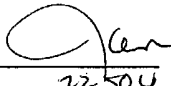
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AA Sequences: ☒ \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: ☒ \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

Search commercial, issued and interference databases.

Thanks,  
Nirmal S. Basi

Searcher:   
Phone: 22504  
Location: \_\_\_\_\_  
Date Picked Up: 4/20  
Date Completed: 6/20  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: 10  
Online time: 60

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: ☒  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
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VENDOR/COST (where applic.)

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Other (specify): \_\_\_\_\_

Sequence 8, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 10, Appli  
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Sequence 69, Appli

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45 1200.5 42.8 677 14

ALIGNMENTS

RESULT 1  
US-10-198-785-2  
Sequence 2, Application US/10198785  
Publication No. US20030022224A1  
GENERAL INFORMATION:  
APPLICANT: OLYMPUS OPTICAL CO., LTD.  
TITLE OF INVENTION: Method of detecting binding reaction between protein and test su  
FILE REFERENCE: 7E1-02S0538  
CURRENT FILING DATE: 2002-07-19  
PRIOR FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: JP/2001-220444  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: JP/2001-221963  
PRIOR FILING DATE: 2001-07-23  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-198-785-2

Query Match	100.0%	Score 2805	DB 14	Length 530
Best Local Similarity	100.0%	Pred. No. 2.1e-254		
Matches 530	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: June 20, 2004, 10:38:43 ; Search time 49 Seconds  
(without alignments)  
3053.597 Million cell updates/sec  
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Perfect score: 2805  
Sequence: 1 MDIKNSPSSLSNPSSSYNCSQ.....ECSPAEDSKSKESQNSQSQSQ 530  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1163542 seqs, 282313646 residues  
Total number of hits satisfying chosen parameters: 1163542  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*\*  
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2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2805	100.0	530	14	US-10-198-785-2
2	2805	100.0	530	14	US-10-157-031-106
3	2805	100.0	530	14	US-10-392-274-4
4	2554	91.1	485	14	US-10-278-481-3
5	2476.5	88.3	555	14	US-10-373-271-1
6	2291	81.7	485	14	US-10-278-481-2
7	2286	81.5	484	14	US-10-278-481-13
8	2267	80.8	485	14	US-10-278-481-5
9	2262	80.6	484	14	US-10-278-481-14
10	2017	71.9	384	14	US-10-278-481-15
11	1235.5	44.0	595	15	US-10-148-835-5
12	1233.5	44.0	595	9	US-09-853-033-2
13	1233.5	44.0	595	15	US-10-148-835-1
14	1233.5	44.0	595	15	US-10-148-835-2
15	1233.5	44.0	595	15	US-10-148-835-9

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RESULT 2  
US-10-157-031-106  
; Sequence 106, Application US/10157031  
; Publication No. US20030108890A1  
; GENERAL INFORMATION:  
; APPLICANT: Baranova, A. V.  
; APPLICANT: Yankovsky, N. K.  
; APPLICANT: Kozlov, A. P.  
; APPLICANT: Lobahev, A. V.  
; APPLICANT: Krukovskaya, L. L.  
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences  
; FILE REFERENCE: 2760-103  
; CURRENT APPLICATION NUMBER: US/10/157,031  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 415  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 106  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-031-106

Query Match 100.0%; Score 2805; DB 14; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.1e-254;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-10-392-274-4  
; Sequence 4, Application US/10392274  
; Publication No. US20030199472A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-HENDY, AYMAN  
; APPLICANT: LEE, EUN JIG  
; APPLICANT: JAMESON, J. LARRY  
; TITLE OF INVENTION: ADENOVIRUS-MEDIATED THERAPY FOR UTERINE FIBROIDS  
; FILE REFERENCE: UTSG:252USPI  
; CURRENT APPLICATION NUMBER: US/10/392,274  
; CURRENT FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-392-274-4

Query Match 100.0%; Score 2805; DB 14; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.1e-254;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 CKNVVFPVYDILLEMLNAHVLRGCKSSITGSECSFPAEDSKSKEGSPQSQ 530

RESULT 4

US-10-278-481-3  
; Sequence 3, Application US/10278481  
; Publication No. US20030113803A1  
; GENERAL INFORMATION:  
; APPLICANT: K&O BIO AB  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; STREET: c/o Center for Biotechnology and Department  
; of Medical Nutrition, Karolinska  
; Institute  
; CITY: Huddinge  
; COUNTRY: Sweden  
; ZIP: S-14186  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/278,481  
; FILING DATE: 23-Oct-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/333,057  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/836,620  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: GB 9518272.1  
; FILING DATE: 08-SEP-1995  
; APPLICATION NUMBER: GB 9605550.4  
; FILING DATE: 15-MAR-1996  
; APPLICATION NUMBER: GB 9607532.0  
; FILING DATE: 11-APR-1996  
; APPLICATION NUMBER: GB 9609576.5  
; FILING DATE: 08-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GUSTAFSSON, Jan-Ake  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-278-481-3

Query Match 91.1%; Score 2554; DB 14; Length 485;  
Best Local Similarity 99.8%; Pred. No. 7.2e-23i;  
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Qy 166 CEGCKAFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVCKGSRRCRG 225  
Db 121 CEGCKAFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVCKGSRRCRG 180  
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Db 181 YRLVRQRSADEQLHCAGKAKRSGGHAPRVRELLDALSPPQLVTLLEAPPHVLSRP 240  
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Db 241 SAPFTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCKWMEVLMGLMW 300

Qy 346 RSIDHPGKLIIPAPDLVLRDDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMIL 405

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Db 421 RHASNKGEHLLNMCKKNVFPVYDILLEMLNAHVLRGCKSSITGSECSFPAEDSKSKEG 480

Qy 526 NPQSQ 530

Db 481 NLQSQ 485

RESULT 5

US-10-373-271-1  
; Sequence 1, Application US/10373271  
; Publication No. US20030162257A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Quinet, Elaine M.  
; APPLICANT: Pan, Ermei  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding a No. US20030162257A1e1 Estrogen  
; FILE OF INVENTION: Variant  
; FILE REFERENCE: AM100361  
; CURRENT APPLICATION NUMBER: US/10/373,271  
; CURRENT FILING DATE: 2003-02-25  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 555  
; TYPE: PRT  
; ORGANISM: human testis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (534)..(534)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (542)..(545)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-373-271-1

Query Match 88.3%; Score 2476.5; DB 14; Length 555;  
Best Local Similarity 92.4%; Pred. No. 1.7e-23;  
Matches 477; Conservative 4; Mismatches 14; Indels 21; Gaps 3;

Qy 1 MDIKNSPSSILNSPSSYNCQSILPLEHSGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
Db 11 MNKNSPSSILNSPSSYNCQSILPLEHSGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 70  
Qy 61 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPOKSPWCEARSLEHTLPVN 120  
Db 71 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPOKSPWCEARSLEHTLPVN 130  
Qy 121 RETLKRVSGNRCSAPVTPGSKRDHFCVCSVDYASGYHGWSCGCKAFKRSIQGH 180  
Db 131 RETLKRVSGNRCSAPVTPGSKRDHFCVCSVDYASGYHGWSCGCKAFKRSIQGH 190  
Qy 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVCKGSRRCRGYRLVRQRSADEQLH 240  
Db 191 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVCKGSRRCRGYRLVRQRSADEQLH 250  
Qy 241 CAGKAKRSGGHAPRVRELLDALSPPQLVTLLEAPPHVLSRPAPFTEASMMSLTK 300  
Db 251 CAGKAKRSGGHAPRVRELLDALSPPQLVTLLEAPPHVLSRPAPFTEASMMSLTK 310  
Qy 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCKWMEVLMGLMWSDHPGKLIIPAPDL 360

Db 311 LADKELVHMISWAKIPGPFVLSLFDQVRLLESCHWMEVLMGLMNRSIDHPGKLIAPD 370  
 Qy 361 VLDRDGGKCVGILEIFDMLATTSSRFELKQHKYLCVKAMILLNNSWYPLVATODA 420  
 Db 371 VLDRDGGKCVGILEIFDMLATTSSRFELKQHKYLCVKAMILLNNSWYPLVATODA 430  
 Qy 421 DSRKLAHLINAVTDALVWVIAKSGISSQQSMLANLMLLSHVPHASNKGMHLLMK 480  
 Db 431 DSRKLAHLINAVTDALVWVIAKSGISSQQSMLANLMLLSHVPHAR----- 479  
 Qy 481 CKNVVYDILLLEMLNA--HVLRGCKSSITGSCSP 514  
 Db 480 -----LYIWLAKMFAALKOILRAPFS--SRECFP 507

## RESULT 6

US-10-278-481-2  
 ; Sequence 2, Application US/10278481  
 ; Publication No. US20030113803A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KARO BIO AB  
 ; TITLE OF INVENTION: Orphan receptor  
 ; NUMBER OF SEQUENCES: 19  
 ; STREET: c/o Center for Biotechnology and Department  
 ; of Medical Nutrition, Karolinska Nutrition, Karolinska  
 ; Institute  
 ; CITY: Huddinge  
 ; COUNTRY: Sweden  
 ; ZIP: S-14186  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/278,481  
 ; FILING DATE: 23-Oct-2002  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/333,057  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/836,620  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: GB 9518272.1  
 ; FILING DATE: 08-SEP-1995  
 ; APPLICATION NUMBER: GB 9605550.4  
 ; FILING DATE: 15-MAR-1996  
 ; APPLICATION NUMBER: GB 9607532.0  
 ; FILING DATE: 11-APR-1996  
 ; APPLICATION NUMBER: GB 9609576.5  
 ; FILING DATE: 08-MAY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GUSTAFSSON, Jan-Ake  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 485 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; ORGANISM: Rattus rattus  
 ; ORIGINAL SOURCE:  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-278-481-2

Query Match 81.7%; Score 2291; DB 14; Length 485;  
 Best Local Similarity 88.7%; Pred. No. 3.8e-206;  
 Matches 430; Conservative 23; Mismatches 32; Indels 0; Gaps 0;  
 Qy 46 MTFYSPAVMNYISNVNTEGGPGROTTSPNVLWPTPGHLSPVLVHRQLSHLYAEPOKS 105  
 Db 1 MTFYSPAVMNYSVRGTSNLDGGPVLSTSPNVLWPTSGHLSPLATHCQSSLLYAEPOKS 60  
 Qy 106 PWCARSLEHTLPVNRRETLKPKVGNCRKASPVTPGSGKRDPAHFCVACSDYASGHYGVWS 165  
 Db 61 PWCARSLEHTLPVNRRETLKPKVGNCRKASPVTPGSGKRDPAHFCVACSDYASGHYGVWS 120

Qy 166 CEGCKAPFKRSIQGHNDYICPATNOCTIDKNRRKSCQAQLRKCYEVGMVKGSRRCG 225  
 Db 121 CEGCKAPFKRSIQGHNDYICPATNOCTIDKNRRKSCQAQLRKCYEVGMVKGSRRCG 180  
 Qy 226 YRLVROSSADSOQLHCAKAKXSGGHAPRVRELLDALSPQLVLTLEAPPVHLISRP 285  
 Db 181 YRLVROSSADSOQLHCAKAKXSGGHAPRVRELLDALSPQLVLTLEAPPVHLISRP 240  
 Qy 286 SAPPTASMMASLTAKLADKELVHMISWAKIPGPFVLSLFDQVRLLESCHWMEVLMGLMW 345  
 Db 241 SMPPTASMMASLTAKLADKELVHMISWAKIPGPFVLSLFDQVRLLESCHWMEVLMGLMW 300  
 Qy 346 RSIDHPGKLIAPDVLDRDGGKCVGILEIFDMLATTSSRFELKQHKYLCVKAMIL 405  
 Db 301 RSIDHPGKLIAPDVLDRDGGKCVGILEIFDMLATTSSRFELKQHKYLCVKAMIL 360  
 Qy 406 LNNSWYPLVATODADSRKLAHLINAVTDALVWVIAKSGISSQQSMLANLMLLSHV 465  
 Db 361 LNNSWYPLASANQEAESRSKLTLLINAVTDALVWVIAKSGISSQQSMLANLMLLSHV 420  
 Qy 466 RHASNKGMHLLMKCKNVVYDILLLEMLNAHVLRGCKSSITGSCSPADSKSGSQ 525  
 Db 421 RHISNKGMEHLLSMCKNVVYDILLLEMLNAHVLRGCKSSITGSCSPADSKSGSQ 480  
 Qy 526 NPQSQ 530  
 Db 481 NLQSQ 485

## RESULT 7

US-10-278-481-13  
 ; Sequence 13, Application US/10278481  
 ; Publication No. US20030113803A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KARO BIO AB  
 ; TITLE OF INVENTION: Orphan receptor  
 ; NUMBER OF SEQUENCES: 19  
 ; STREET: c/o Center for Biotechnology and Department  
 ; of Medical Nutrition, Karolinska Nutrition, Karolinska  
 ; Institute  
 ; CITY: Huddinge  
 ; COUNTRY: Sweden  
 ; ZIP: S-14186  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/278,481  
 ; FILING DATE: 23-Oct-2002  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/333,057  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/836,620  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: GB 9518272.1  
 ; FILING DATE: 08-SEP-1995  
 ; APPLICATION NUMBER: GB 9605550.4  
 ; FILING DATE: 15-MAR-1996  
 ; APPLICATION NUMBER: GB 9607532.0  
 ; FILING DATE: 11-APR-1996  
 ; APPLICATION NUMBER: GB 9609576.5  
 ; FILING DATE: 08-MAY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GUSTAFSSON, Jan-Ake  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 484 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; ORIGINAL SOURCE:

ORGANISM: Rattus rattus  
SEQUENCE DESCRIPTION: SEQ ID NO: 13;  
US-10-278-481-13

Query Match 81.5%; Score 2286; DB 14; Length 484;  
Best Local Similarity 88.6%; Pred. No. 1.1e-205;  
Matches 429; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

QY 46 MTFYSPAVMYSPISPNVNLGGPGROTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKS 105  
DB 1 MTFYSPAVMYSPVPOSTNLOGPVLSTSPNVLWPTSGHLSPLATHCQSSLLYAEPOKS 60

QY 106 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSKRDHAFCAVCSYASGTHYGVWS 165  
DB 61 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSKRDHAFCAVCSYASGTHYGVWS 120

QY 166 CEGKAFKRSIQGHNDYICPATNOCITDKNRKSCQACRLKCYEVMVKCGSRRERCG 225  
DB 121 CEGKAFKRSIQGHNDYICPATNOCITDKNRKSCQACRLKCYEVMVKCGSRRERCG 180

QY 226 YRLVRRORSADQLHCAGKAGSGHAPRVRELLDALSPQLVLTLEAPPHVLSRP 285  
DB 181 YRLVRRORSADQLHCAGKAGSGHAPRVRELLDALSPQLVLTLEAPPHVLSRP 240

QY 286 SAPTEASMMSLTKLADKELVHMSWAKKIPGVFVLSLFDVRLLESCHWVLMGLMW 345  
DB 241 SMPTEASMMSLTKLADKELVHMSWAKKIPGVFVLSLFDVRLLESCHWVLMGLMW 300

QY 346 RSIDHPGKLIIPADVLDRDECKVEGILEIFDMLLATTSFRELKQKCYLCVKAMIL 405  
DB 301 RSIDHPGKLIIPADVLDRDECKVEGILEIFDMLLATTSFRELKQKCYLCVKAMIL 360

QY 406 LNSSMYPLVTATODASRKLHLNNAVTDALVWVIAKSGISSQOOSRLANLMLLSHV 465  
DB 361 LNSSMYPLVTATODASRKLHLNNAVTDALVWVIAKSGISSQOOSRLANLMLLSHV 420

QY 466 RHASNKGHEHLNMMCKNVVPPVYDILLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 525  
DB 421 RHISNKGHEHLNMMCKNVVPPVYDILLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 480

QY 526 NPQS 529  
DB 481 NLQS 484

RESULT 8  
US-10-278-481-5  
Sequence 5, Application US/10278481  
Publication No. US20030113803A1  
GENERAL INFORMATION:  
APPLICANT: KARO BIO AB  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska Nutrition, Karolinska Institute  
CITY: Huddinge  
COUNTRY: Sweden  
ZIP: S-14186

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/278,481  
FILING DATE: 23-Oct-2002

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/333,057  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/836,620  
FILING DATE: <Unknown>  
APPLICATION NUMBER: GB 9518272.1

FILING DATE: 08-SEP-1995  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996

ATTORNEY/AGENT INFORMATION:  
NAME: GUSTAFSSON, Jan-Ake  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORGANISM: Mus musculus  
SEQUENCE DESCRIPTION: SEQ ID NO: 5;  
US-10-278-481-5

Query Match 80.8%; Score 2267; DB 14; Length 485;  
Best Local Similarity 88.0%; Pred. No. 6.8e-204;  
Matches 427; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 46 MTFYSPAVMYSPISPNVNLGGPGROTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKS 105  
DB 1 MAFYSPAVMYSPVSSITGNLEGGPVQTASPNVLWPTSGHLSPLATHCQSSLLYAEPOKS 60

QY 106 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSKRDHAFCAVCSYASGTHYGVWS 165  
DB 61 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSKRDHAFCAVCSYASGTHYGVWS 120

QY 166 CEGKAFKRSIQGHNDYICPATNOCITDKNRKSCQACRLKCYEVMVKCGSRRERCG 225  
DB 121 CEGKAFKRSIQGHNDYICPATNOCITDKNRKSCQACRLKCYEVMVKCGSRRERCG 180

QY 226 YRLVRRORSADQLHCAGKAGSGHAPRVRELLDALSPQLVLTLEAPPHVLSRP 285  
DB 181 YRLVRRORSADQLHCAGKAGSGHAPRVRELLDALSPQLVLTLEAPPHVLSRP 240

QY 286 SAPTEASMMSLTKLADKELVHMSWAKKIPGVFVLSLFDVRLLESCHWVLMGLMW 345  
DB 241 SMPTEASMMSLTKLADKELVHMSWAKKIPGVFVLSLFDVRLLESCHWVLMGLMW 300

QY 346 RSIDHPGKLIIPADVLDRDECKVEGILEIFDMLLATTSFRELKQKCYLCVKAMIL 405  
DB 301 RSIDHPGKLIIPADVLDRDECKVEGILEIFDMLLATTSFRELKQKCYLCVKAMIL 360

QY 406 LNSSMYPLVTATODASRKLHLNNAVTDALVWVIAKSGISSQOOSRLANLMLLSHV 465  
DB 361 LNSSMYPLVTATODASRKLHLNNAVTDALVWVIAKSGISSQOOSRLANLMLLSHV 420

QY 466 RHASNKGHEHLNMMCKNVVPPVYDILLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 525  
DB 421 RHISNKGHEHLNMMCKNVVPPVYDILLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 480

QY 526 NPQS 530  
DB 481 NLQS 485

RESULT 9  
US-10-278-481-14  
Sequence 14, Application US/10278481  
Publication No. US20030113803A1  
GENERAL INFORMATION:  
APPLICANT: KARO BIO AB  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska Nutrition, Karolinska Institute  
CITY: Huddinge  
COUNTRY: Sweden

Sun Jun 20 11:32:41 2004

ZIP: S-14186  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
FILING DATE: 23-Oct-2002  
APPLICATION NUMBER: US/10/278,481  
FILING DATE: 23-Oct-2002  
APPLICATION NUMBER: US/09/333,057  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/836,620  
FILING DATE: <Unknown>  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GUSTAFSSON, Jan-Ake  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 484 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-278-481-14

Query Match 80.6%; Score 2262; DB 14; Length 484;  
Best Local Similarity 88.0%; Pred. No. 2e-203;  
Matches 426; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY	46	MTFSPVAVMYSPISNVNTEGGPGRTTSPNVLWPTGHLSPVVRQLSHLYAPQKS	105
DB	1	MAFISPAVMYSPVSSNLEGGPVQRTASPNVLWPTSGHLSPLATHCQSSLLYAPQKS	60
QY	106	PWCEARSLHTLPVNRRTLRKVSGNRCASPVTPGSKRDRAHCAVCSYASGYHYGWS	165
DB	61	PWCEARSLHTLPVNRRTLRKVSGNRCASPVTPGSKRDRAHCAVCSYASGYHYGWS	120
QY	166	CEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACRLKCYEVMVKCGSRRCG	225
DB	121	CEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACRLKCYEVMVKCGSRRCG	180
QY	226	YRLVRRQRSADQLHCAGKACRSCHAPRVRELLDALSPEQLVLTLLREAPPVHLISRP	285
DB	181	YRLVRRQRSADQLHCAGKACRSCHAPRVRELLDALSPEQLVLTLLREAPPVHLISRP	240
QY	286	SAPTEASMMSLTKLADKELVHMSWAKIPGVVLSLDDQVRLLESQWVLMVGLMW	345
DB	241	SMPTEASMMSLTKLADKELVHMSWAKIPGVVLSLDDQVRLLESQWVLMVGLMW	300
QY	346	RSIDHPGKLIAPADVLDRDEGKCVGILFIDFMLATTFRFRELKLQHKYELCVKAMIL	405
DB	301	RSIDHPGKLIAPADVLDRDEGKCVGILFIDFMLATTFRFRELKLQHKYELCVKAMIL	360
QY	406	LNSNWPVLTATQADSRKLAHLNNAVTALVWVIAKSGISSQOOSMRLLNMLLSHV	465
DB	361	LNSNWPVLTATQADSRKLAHLNNAVTALVWVIAKSGISSQOOSMRLLNMLLSHV	420
QY	466	RHASNKGHEHLNKNVPPVYDILLEMNAHVLRGCKSSITGSECSPAEDSKSKEGQ	525
DB	421	RHASNKGHEHLNKNVPPVYDILLEMNAHVLRGCKSSITGSECSPAEDSKSKEGQ	480
QY	526	NPOS 529	
DB	481	NLOS 484	

RESULT 10  
US-10-278-481-15  
Sequence 15, Application US/10278481  
Publication No. US20030113803A1  
GENERAL INFORMATION:  
APPLICANT: KARO BIO AB  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
STREET: c/o Center for Biotechnology and Department  
of Medical Nutrition, Karolinska Nutrition, Karolinska  
Institute  
CITY: Huddinge  
COUNTRY: Sweden  
ZIP: S-14186  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/278,481  
FILING DATE: 23-Oct-2002  
APPLICATION NUMBER: US/09/333,057  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/836,620  
FILING DATE: <Unknown>  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GUSTAFSSON, Jan-Ake  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 384 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-278-481-15

Query Match 71.9%; Score 2017; DB 14; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.5e-180;  
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	86	LSPLVVRQLSHLYABPQKSPWCEARSLHTLPVNRRTLRKVSGNRCASPVTPGSKRD	145
DB	2	LSPLVVRQLSHLYABPQKSPWCEARSLHTLPVNRRTLRKVSGNRCASPVTPGSKRD	61
QY	146	AHFCVCSYASGYHYGWSCEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACR	205
DB	62	AHFCVCSYASGYHYGWSCEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACR	121
QY	206	LKRCYEVGMVKCGSRRCRGYRLVRRQRSADQLHCAGKACRSCHAPRVRELLDALS	265
DB	122	LKRCYEVGMVKCGSRRCRGYRLVRRQRSADQLHCAGKACRSCHAPRVRELLDALS	181
QY	266	EQVLVTLLEABPHVLI SRSPAPTEASMMSLTKLADKELVHMSWAKIPGVVLSL	325
DB	182	EQVLVTLLEABPHVLI SRSPAPTEASMMSLTKLADKELVHMSWAKIPGVVLSL	241
QY	326	DOVRLLESQWVLMVGLMWVRSIDHPGKLIAPADVLDRDEGKCVGILFIDFMLATT	385
DB	242	DOVRLLESQWVLMVGLMWVRSIDHPGKLIAPADVLDRDEGKCVGILFIDFMLATT	301



QY 386 REFELKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNNAVTDLVWVIAKSG 445  
 DB 302 REFELKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNNAVTDLVWVIAKSG 361  
 QY 446 ISSQQSQSRLANLMLSHVRHA 468  
 DB 362 ISSQQSQSRLANLMLSHVRHA 384  
 RESULT 11  
 US-10-148-835-5  
 ; Sequence 5, Application US/10148835  
 ; Publication No. US20030207380A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAITO et al.  
 ; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION  
 ; FILE REFERENCE: 2185-0648P  
 ; CURRENT APPLICATION NUMBER: US/10/148,835  
 ; CURRENT FILING DATE: 2002-10-11  
 ; NUMBER OF SEQ ID NOS: 213  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 595  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-148-835-5

Query Match 44.0%; Score 1235.5; DB 15; Length 595;  
 Best Local Similarity 48.4%; Pred. No. 8.2e-107;  
 Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;  
 QY 5 NSPSSINSPSSYNCOSILPLEH--GSIYIPSS--YVDSHHEYDAMTFYSPAVMVSIPS 60  
 DB 21 NELEPLNRP-----OLKIPLERPLGEVILDSKPAVINYFEGAYEFNAANAQAQVYG 74  
 QY 61 NVTNLGGGPGRO-----TTSNVLWPTFGHLSL-LVVRQLSHLYAE 101  
 DB 75 Q-TGLPYGCGSEAAAFSGNLGPPPLNSVSPPLMLLHPPLQSPFLPHGQQVPPYILE 133  
 QY 102 POKSPWC--EARSLEHTLPVNRETLKRKVGNCRCASPVTPGPG-----SKRDAHFCAVCS 154  
 DB 134 NEPSGYTVREAGPPAFYRP---NSDNRQGGRELRLASTNDKGSMAESAKETRYCAVND 190  
 QY 155 YASGVHYGVWSCGCGKAPFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEVC 214  
 DB 191 YASGVHYGVWSCGCGKAPFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEVC 250  
 QY 215 VKGSRRRRCGVRLVRRORSADQLHCAGKAKRSGCHAPVR-----EL 258  
 DB 251 MKGGIRKDRRGGMKHKRQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305  
 QY 259 LLDALSPQLVLTLLAEPPHVLISR--PSAPPTASMMSLTKLADKELVHMIWAKKI 316  
 DB 306 LALSUTADQVMSALLDAEPP-ILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
 QY 317 PGFVELSLFDQVRLLESCEMVEVLMMGLMWRSIDHPGKLI FAPDLVLDREDEGKCVGILBI 376  
 DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSVEHPGKLI FAPNLILDRNQKCVGMEI 424  
 QY 377 FDLMTATTSRFRRLKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNNAVT 435  
 DB 425 FDLMTATTSRFRFMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRLDKITD 484  
 QY 436 ALVWVIAKSGISSQQSQSRLANLMLSHVRHASKMGHEHLNLMKCKNVVPPVYDLLEML 495  
 DB 485 TLHLWAKAGLTQQQHQRLAQALLILSHIRMSNKGHEHLYSMCKKNVPPVYDLLEML 544  
 QY 496 NAHVL 500  
 DB 545 DAHRL 549

RESULT 12

US-09-853-033-2  
 ; Sequence 2, Application US/09853033  
 ; Patent No. US20020100068A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMON, PIERRE  
 ; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION  
 ; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER  
 ; FILE REFERENCE: 065691/0222  
 ; CURRENT APPLICATION NUMBER: US/09/853,033  
 ; CURRENT FILING DATE: 2001-05-11  
 ; PRIOR APPLICATION NUMBER: FR 00/12570  
 ; PRIOR FILING DATE: 2000-10-03  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 595  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-853-033-2  
 Query Match 44.0%; Score 1233.5; DB 9; Length 595;  
 Best Local Similarity 48.4%; Pred. No. 1.3e-106;  
 Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;  
 QY 5 NSPSSINSPSSYNCOSILPLEH--GSIYIPSS--YVDSHHEYDAMTFYSPAVMVSIPS 60  
 DB 21 NELEPLNRP-----OLKIPLERPLGEVILDSKPAVINYFEGAYEFNAANAQAQVYG 74  
 QY 61 NVTNLGGGPGRO-----TTSNVLWPTFGHLSL-LVVRQLSHLYAE 101  
 DB 75 Q-TGLPYGCGSEAAAFSGNLGPPPLNSVSPPLMLLHPPLQSPFLPHGQQVPPYILE 133  
 QY 102 POKSPWC--EARSLEHTLPVNRETLKRKVGNCRCASPVTPGPG-----SKRDAHFCAVCS 154  
 DB 134 NEPSGYTVREAGPPAFYRP---NSDNRQGGRELRLASTNDKGSMAESAKETRYCAVND 190  
 QY 155 YASGVHYGVWSCGCGKAPFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEVC 214  
 DB 191 YASGVHYGVWSCGCGKAPFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEVC 250  
 QY 215 VKGSRRRRCGVRLVRRORSADQLHCAGKAKRSGCHAPVR-----EL 258  
 DB 251 MKGGIRKDRRGGMKHKRQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305  
 QY 259 LLDALSPQLVLTLLAEPPHVLISR--PSAPPTASMMSLTKLADKELVHMIWAKKI 316  
 DB 306 LALSUTADQVMSALLDAEPP-ILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
 QY 317 PGFVELSLFDQVRLLESCEMVEVLMMGLMWRSIDHPGKLI FAPDLVLDREDEGKCVGILBI 376  
 DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSVEHPGKLI FAPNLILDRNQKCVGMEI 424  
 QY 377 FDLMTATTSRFRRLKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNNAVT 435  
 DB 425 FDLMTATTSRFRFMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRLDKITD 484  
 QY 436 ALVWVIAKSGISSQQSQSRLANLMLSHVRHASKMGHEHLNLMKCKNVVPPVYDLLEML 495  
 DB 485 TLHLWAKAGLTQQQHQRLAQALLILSHIRMSNKGHEHLYSMCKKNVPPVYDLLEML 544  
 QY 496 NAHVL 500  
 DB 545 DAHRL 549  
 RESULT 13  
 US-10-148-835-1  
 ; Sequence 1, Application US/10148835  
 ; Publication No. US20030207380A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAITO et al.  
 ; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

```
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-1

Query Match      44.0%; Score 1233.5; DB 15; Length 595;
Best Local Similarity 48.4%; Pred. No. 1.3e-106;
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;

QY 5 NSPSSLNSPSSVNCYSQSIPLLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMYSIPS 60
DB 21 NELEPLNRP-----QLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAAAQAQVYG 74
QY 61 NVTNLEGGPGRQ-----TTSNVLMPTPGHLSPL-LVVRQLSHLYAE 101
DB 75 Q-TGLPYGPGSEAAAFSGNSGLGFPPLNSVSPPLMLLHPPLQSPPLQPHGQOVPYYLE 133
QY 102 POKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPGP-----SKDAHFCAVCS 154
DB 134 NEPSGTYVREAGPPAFYRP---NSDNRQGRERLASTNDKSGMAMESAKETRYCAVCND 190
QY 155 YASGYHYGVMSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEUGM 214
DB 191 YASGYHYGVMSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEUGM 250
QY 215 VKGSRERCGYRLVRRQSADEQLHCAGKAKRSKGHAPRV-----REL 258
DB 251 MKGGIRKDRGGRMUKHKQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305
QY 259 LLDALSPQVLTLLEAEPPHYLISR--PSAPPTTEASMMSLTKADKELVHMISWAKKI 316
DB 306 LALSITADQVMSALEDAEPP-ILYSEYDPTRPFSSEASMMGLLTNLADRELVMINWAKRV 364
QY 317 PGFVELSLFDQVRLLESCEWELMMGLMWSIDHPGKLIPAPDLVLDROGKCVGEILEI 376
DB 365 PGFVDLTLDQVHLLECAWLEILMGLVWRSMEHPGKLLFAPNLLLDENQKCVGEVVEI 424
QY 377 FDMLLATTSRPRELKLQHKYLCVKAMILLNSMYPVLTAT-QDADSSRKLHLNAVTD 435
DB 425 FDMLLATTSRPRMNLQGEFVCLKSIILNSGVYTFSLTSLKSLEEKDHIHRVLDKITD 484
QY 436 ALVWVIAKSGISSQQSOMRLANILMLLSHVHASNKGWEHLNKKCNVVPVYDILLLEML 495
DB 485 TLILHMAKAGLTQQOQHQAQLLLILSHIRHNSKNKGWEHLNKKCNVVPVYDILLLEML 544
QY 496 NAHVL 500
DB 545 DAHRL 549

RESULT 15
US-10-148-835-2
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2

Query Match      44.0%; Score 1233.5; DB 15; Length 595;
Best Local Similarity 48.4%; Pred. No. 1.3e-106;
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;

QY 5 NSPSSLNSPSSVNCYSQSIPLLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMYSIPS 60
DB 21 NELEPLNRP-----QLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAAAQAQVYG 74
QY 61 NVTNLEGGPGRQ-----TTSNVLMPTPGHLSPL-LVVRQLSHLYAE 101
DB 75 Q-TGLPYGPGSEAAAFSGNSGLGFPPLNSVSPPLMLLHPPLQSPPLQPHGQOVPYYLE 133
QY 102 POKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPGP-----SKDAHFCAVCS 154
DB 134 NEPSGTYVREAGPPAFYRP---NSDNRQGRERLASTNDKSGMAMESAKETRYCAVCND 190
QY 155 YASGYHYGVMSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEUGM 214
DB 191 YASGYHYGVMSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEUGM 250
QY 215 VKGSRERCGYRLVRRQSADEQLHCAGKAKRSKGHAPRV-----EL 258
DB 251 MKGGIRKDRGGRMUKHKQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305
QY 259 LLDALSPQVLTLLEAEPPHYLISR--PSAPPTTEASMMSLTKADKELVHMISWAKKI 316
DB 306 LALSITADQVMSALEDAEPP-ILYSEYDPTRPFSSEASMMGLLTNLADRELVMINWAKRV 364
QY 317 PGFVELSLFDQVRLLESCEWELMMGLMWSIDHPGKLIPAPDLVLDROGKCVGEILEI 376
DB 365 PGFVDLTLDQVHLLECAWLEILMGLVWRSMEHPGKLLFAPNLLLDENQKCVGEVVEI 424
QY 377 FDMLLATTSRPRELKLQHKYLCVKAMILLNSMYPVLTAT-QDADSSRKLHLNAVTD 435
DB 425 FDMLLATTSRPRMNLQGEFVCLKSIILNSGVYTFSLTSLKSLEEKDHIHRVLDKITD 484
QY 436 ALVWVIAKSGISSQQSOMRLANILMLLSHVHASNKGWEHLNKKCNVVPVYDILLLEML 495
DB 485 TLILHMAKAGLTQQOQHQAQLLLILSHIRHNSKNKGWEHLNKKCNVVPVYDILLLEML 544
QY 496 NAHVL 500
DB 545 DAHRL 549

RESULT 14
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2
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Db 75 Q-TGLPYGFGSAAAFNGNLGGPPPLNSVSPPLMLLHPPQLSPFFLOPHGQQVPPYLE 133  
Qy 102 POKSEWC--EARSLEHTLTVNRETILKRVSGNRKASPVTFGP-----SKRDAHFCVACSD 154  
Db 134 NEPSGYTVREAGPPAFYRP---NSDNRRQGGRERLASTNDKSGMAMESAKETRYCAVCND 190  
Qy 155 YASGYHYGWSCEGCKAFKRSIOGHNDYICPATNCTIDKNRKSCQACBLRKCIEYGM 214  
Db 191 YASGYHYGWSCEGCKAFKRSIOGHNDYICPATNCTIDKNRKSCQACBLRKCIEYGM 250  
Qy 215 VKGSRRCRGYRLVRRORSADQLHFCAGKAKRSGCHAPVR-----EL 258  
Db 251 MKGGIRKDRRGGRMLKHKKQRDD-----GEGRGEVGSAGDMAANLWSPPLMIKESKNS 305  
Qy 259 LLDALSPQLVLTLEABPPHVLISR--PSAPFTASMMMSLTKLADKELVHMISWAKI 316  
Db 306 LALSITADQMSALIDABPP-ILYSEYDPTRPFSASMMGLLTNLADRELVMINWAKRV 364  
Qy 317 PGFVELSLPDOVRILLESQWMEVLMWGLMWRSIDHPKLI FAPDLVLDREBKGKVEGILEI 376  
Db 365 PGFVDTLHDQVHLLCACWLEILMIGLVWRSMEHPKLLFAPNLULLDRNQKCVGVEI 424  
Qy 377 FDMLLATTSRPRELKLQHKYLCVKAMILLNSMYPLVTAT-ODADSSRKLAHLINAVTD 435  
Db 425 FDMLLATTSRPRMNLQGBEFVCLAKIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKTD 484  
Qy 436 ALVWVIKSGISSQOSMELANLMLLSHVHASNKGMEHLNMMCKKNWVPYDLLLLLML 495  
Db 485 TLHLMKAGLTLOQOQHQLAQLLLILSHIRMSNRKMEHLYSMCKKNWVPYDLLLLLML 544  
Qy 496 NAHVL 500  
Db 545 DAHRL 549

Search completed: June 20, 2004, 10:44:38  
Job time : 50 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:30:42 ; Search time 59 Seconds  
(without alignments)  
2538.139 Million cell updates/sec

Title: US-08-906-365-2  
Perfect score: 2805  
Sequence: 1 MDIKNSPSSLSNPSYNSQ.....ECSFADSKSKEGSONPQSQ 530

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2805	100.0	530	2	Aaw33215 Human oes
2	2805	100.0	530	2	Aaw37858 Human oes
3	2805	100.0	530	4	Aab60649 Human oes
4	2805	100.0	530	4	Aau27322 Human oes
5	2805	100.0	530	4	Aae10457 Human est
6	2805	100.0	530	5	Aab47835 Full leng
7	2805	100.0	530	5	Abg32754 Nuclear r
8	2805	100.0	530	6	Ad83824 Human BSR
9	2805	100.0	530	6	Abu61828 Human oes
10	2805	100.0	530	7	Ad812138 Human oes
11	2805	100.0	548	2	Aay07270 Human oes
12	2805	100.0	793	5	Abb80756 Amino aci
13	2554	91.1	485	2	Aaw14724 Human oes
14	2535	90.4	485	2	Aay01597 An estrog
15	2522	89.9	477	2	Aaw33212 Human oes
16	2522	89.9	477	5	Aab47834 Estrogen
17	2502	89.2	549	2	Aaw98125 Mouse oes
18	2500	89.1	549	2	Aay04434 Murine mE
19	2487.5	88.7	495	6	Abj72350 Human oes
20	2481	88.4	567	2	Aaw98128 Mouse com
21	2457	87.6	560	2	Aay04433 Murine mE
22	2391	81.7	485	2	Aaw14723 Rat oestr
23	2291	81.7	485	2	Aay01596 An estrog
24	2267	80.8	485	2	Aaw14725 Mouse oes
25	2245.5	80.1	510	2	Aaw98126 Mouse oes

26	2245.5	80.1	510	2	AAY04435	AAY04435 Murine mE
27	2231.5	79.6	474	3	AAY51946	AAY51946 Bovine ER
28	2198	78.4	416	2	AAW33213	AAW33213 Human oes
29	2198	78.4	416	5	AAB47837	AAB47837 ER splice
30	2198	78.4	418	2	AAW33214	AAW33214 Human oes
31	2198	78.4	418	5	AAB47836	AAB47836 ER splice
32	1746	62.2	414	2	AAW98127	AAW98127 Rat oestr
33	1746	62.2	730	2	AAY04436	AAY04436 Rat rER b
34	1723	61.4	323	6	ABJ72352	ABJ72352 Human oes
35	1636	58.3	320	5	ABG32755	ABG32755 Nuclear r
36	1363	48.6	268	6	ABU08038	ABU08038 Human ste
37	1235.5	44.0	581	5	ABB83791	ABB83791 Chemidoph
38	1235.5	44.0	595	4	AAG84509	AAG84509 Human oes
39	1233.5	44.0	595	2	AAY21626	AAY21626 Ligand bi
40	1233.5	44.0	595	4	AAG84505	AAG84505 Human oes
41	1233.5	44.0	595	4	AAG84513	AAG84513 Human oes
42	1233.5	44.0	595	4	AAG84506	AAG84506 Human oes
43	1233.5	44.0	595	5	ABB76378	ABB76378 Human nuc
44	1231.5	43.9	595	4	AAG84512	AAG84512 Human oes
45	1230.5	43.9	595	4	AAG84507	AAG84507 Human oes

## ALIGNMENTS

## RESULT 1

AAW33215  
ID AAW33215 standard; protein; 530 AA.

AC AAW33215;

XX 20-APR-1998 (first entry)

DT Human oestrogen receptor protein #2.

DE Human oestrogen receptor protein #2.

XX Oestrogen receptor protein; steroid; alternative splicing; estradiol;

XX estone; estradiol; screening.

XX Homo sapiens.

XX EP798378-A2.

XX 01-OCT-1997.

XX 25-MAR-1997; 97EP-00200903.

XX 26-MAR-1996; 96EP-00200820.

XX 22-NOV-1996; 96EP-00203284.

XX (ALKU ) AKZO NOBEL NV.

XX Mosselman S, Dijkema R;

XX WPI; 1997-473188/44.

XX N-PSDB; AAT88415.

XX DNA encoding estrogen receptor - useful in screening assay to identify

XX novel ligands or hormonal analogues.

XX Claim 4; Page 35-37; 45pp; English.

XX This sequence represents a novel oestrogen binding protein isolated from

XX human testis cDNA in order to study upstream translation-initiation

XX codons using 5' RACE-PCR technology. This receptor is able to bind and be

XX activated by estradiol, estone and estriol, can be used in a screening

XX assay for the identification of new drugs e.g. novel ligands or hormonal

XX analogues

XX Sequence 530 AA;

XX Query Match 100.0%; Score 2805; DB 2; Length 530;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-258;

XX Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
 DB 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
 QY 61 NVTNLEGGPGROTTSPNVLPWPTPGHLSPLVVRQLSHLYAEPOKSPKCEARSLEHTLPVN 120  
 DB 61 NVTNLEGGPGROTTSPNVLPWPTPGHLSPLVVRQLSHLYAEPOKSPKCEARSLEHTLPVN 120  
 QY 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180  
 DB 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180  
 QY 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCGSRRCRGYLVVRQRSADQLH 240  
 DB 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCGSRRCRGYLVVRQRSADQLH 240  
 QY 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300  
 DB 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300  
 QY 301 LADKELVHMSWAKKIPGVFELSDFDQVRLLESCEMELANLLMGLMWRSIDHPGKLIAPDL 360  
 DB 301 LADKELVHMSWAKKIPGVFELSDFDQVRLLESCEMELANLLMGLMWRSIDHPGKLIAPDL 360  
 QY 361 VLDRDEGKCEGILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPVLTATODA 420  
 DB 361 VLDRDEGKCEGILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPVLTATODA 420  
 QY 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQMELANLLMGLMWRSIDHPGKLIAPDL 480  
 DB 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQMELANLLMGLMWRSIDHPGKLIAPDL 480  
 QY 481 CKNVVFPYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQNPSQ 530  
 DB 481 CKNVVFPYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQNPSQ 530

## RESULT 2

AAW97858  
 ID AAW97858 standard; protein; 530 AA.

XX AAW97858;

XX 07-JUN-1999 (first entry)

XX Human oestrogen receptor-beta.

XX Oestrogen receptor-beta; HER-beta; human.

XX Homo sapiens.

XX WO9907847-A1.

XX 18-FEB-1999.

XX 20-JUL-1998; 98WO-US014944.

XX 05-AUG-1997; 97US-00906365.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Bhat RA, Henderson RA, Hsiao C, Karathanasis SK;

XX WPI, 1999-167424/14.

XX N-PSDB; AAX24364.

XX Human oestrogen receptor-beta coding sequence - useful in the production  
 of human oestrogen receptor-beta and identification of human oestrogen  
 receptor-beta interactive compounds.

XX Claim 17; Page 42-44; 49pp; English.

XX

CC This polypeptide comprises a full-length human oestrogen receptor-beta  
 (HER-beta), including 45 previously unknown N-terminal amino acid  
 residues that are believed to contribute to the transcription activation  
 function of the receptor. The amino acid sequence was deduced from the  
 nucleotide sequence (see AAX24364) of an isolated cDNA clone. HER-beta is  
 selectively expressed in the thymus, spleen, ovary and testes. The  
 invention encompasses HER-beta polynucleotides and polypeptides,  
 particularly peptides which include residues 1-45 of HER-beta. The  
 invention also provides expression systems in which transcriptionally  
 active HER-beta or fragments can be produced, as well as screening  
 methods for identifying HER-beta agonists and antagonists (including  
 tissue-specific oestrogens and anti-oestrogens), and HER-beta co-  
 activators and inhibitors

XX Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 2; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;  
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
 DB 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
 QY 61 NVTNLEGGPGROTTSPNVLPWPTPGHLSPLVVRQLSHLYAEPOKSPKCEARSLEHTLPVN 120  
 DB 61 NVTNLEGGPGROTTSPNVLPWPTPGHLSPLVVRQLSHLYAEPOKSPKCEARSLEHTLPVN 120  
 QY 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180  
 DB 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180  
 QY 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCGSRRCRGYLVVRQRSADQLH 240  
 DB 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCGSRRCRGYLVVRQRSADQLH 240  
 QY 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300  
 DB 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300  
 QY 301 LADKELVHMSWAKKIPGVFELSDFDQVRLLESCEMELANLLMGLMWRSIDHPGKLIAPDL 360  
 DB 301 LADKELVHMSWAKKIPGVFELSDFDQVRLLESCEMELANLLMGLMWRSIDHPGKLIAPDL 360  
 QY 361 VLDRDEGKCEGILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPVLTATODA 420  
 DB 361 VLDRDEGKCEGILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPVLTATODA 420  
 QY 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQMELANLLMGLMWRSIDHPGKLIAPDL 480  
 DB 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQMELANLLMGLMWRSIDHPGKLIAPDL 480  
 QY 481 CKNVVFPYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQNPSQ 530  
 DB 481 CKNVVFPYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQNPSQ 530

## RESULT 3

AAW60649  
 ID AAW60649 standard; protein; 530 AA.

XX AAW60649;

XX 04-MAY-2001 (first entry)

XX Human oestrogen receptor beta (ER-beta), SEQ ID NO:1.

XX Human oestrogen receptor beta; ER-beta; labelled hormone receptor;  
 optical signal; ligand binding; hormonal disorder;  
 sex hormone associated; ovulation; drug screening; drug discovery.

XX Homo sapiens.

XX

PN WC200107919-A1.  
XX 01-FEB-2001.  
XX 24-JUL-2000; 2000WO-JP004930.  
XX 23-JUL-1999; 99JP-00209860.  
PR 31-MAY-2000; 2000JP-00163475.  
PR 31-MAY-2000; 2000JP-00163476.  
XX (OLYU ) OLYMPUS OPTICAL CO LTD.  
PA Sakamoto H, Kato N;  
XX WPI; 2001-168581/17.  
XX N-PSDB; AAF59897.  
XX Determination of the interaction of a substance for investigation and  
PT diagnosis of hormonal disorders using an optically labelled receptor  
PT protein.  
XX Claim 26; Page 68-72; 75pp; Japanese.  
XX The invention relates to a method for examining the interaction of a test  
CC substance with a hormone receptor protein. The method involves contacting  
CC a test substance with a hormone receptor protein (e.g., an oestrogen  
CC receptor) which is labelled with an optical marker (e.g., a fluorescent  
CC protein), where the marker is capable of undergoing a change in its  
CC optical properties when the receptor binds a ligand. The optical signal  
CC generated in the presence of the test compound is then compared with that  
CC generated in the absence of the test compound to determine whether the  
CC test compound is interacting with the hormone receptor protein. The  
CC invention also encompasses the labelled hormone receptor protein, the  
CC gene encoding it, and vectors and host cells comprising such genes. Of  
CC method of the invention is used for the investigation and diagnosis of  
CC hormonal disorders, especially those associated with sex hormones e.g.,  
CC suppression of ovulation. The present sequence represents human oestrogen  
CC receptor beta (ER-beta)  
XX Sequence 530 AA;  
SQ

Query Match 100.0%; Score 2805; DB 4; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.4e-258; Mismatches 0; Indels 0; Gaps 0;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSINSPSSYNCQSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
DB 1 MDIKNSPSSINSPSSYNCQSILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60  
QY 61 NVTNLEGGPGRTTSNVLWPTPEHLSPLVVRQLSHLYAEPKQSPWCBARSLHTLPVN 120  
DB 61 NVTNLEGGPGRTTSNVLWPTPEHLSPLVVRQLSHLYAEPKQSPWCBARSLHTLPVN 120  
QY 121 RETLKRKVSNGRCASPVTPGSKRAHFAVCSDVASGHHYGVWSCGCKAFPKRSIQGH 180  
DB 121 RETLKRKVSNGRCASPVTPGSKRAHFAVCSDVASGHHYGVWSCGCKAFPKRSIQGH 180  
QY 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEYGVWKCGRRRRCGYRLVRRORSADQLH 240  
DB 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEYGVWKCGRRRRCGYRLVRRORSADQLH 240  
QY 241 CAGKAKRSGGHAPRVRELLDALSPQVLVTLLEAPPHVLISRPSPAPTEASMMWSLTK 300  
DB 241 CAGKAKRSGGHAPRVRELLDALSPQVLVTLLEAPPHVLISRPSPAPTEASMMWSLTK 300  
QY 301 LADKELVEMISWAKIPGFVELSLFDQVALLSCWMEVLMGLMWRSIDHPGKLIAPDL 360  
DB 301 LADKELVEMISWAKIPGFVELSLFDQVALLSCWMEVLMGLMWRSIDHPGKLIAPDL 360  
QY 361 VLDRBEGKCVGILETFDMLATTSPRELKLOHKEYLCVKAMILLNSMYPVLTATQDA 420  
DB 361 VLDRBEGKCVGILETFDMLATTSPRELKLOHKEYLCVKAMILLNSMYPVLTATQDA 420

QY 421 DSSRKLAHLNAVTDALVWVIKSGISSQQSMRIANLLMLLSHVHRASNKMEHLNNK 480  
DB 421 DSSRKLAHLNAVTDALVWVIKSGISSQQSMRIANLLMLLSHVHRASNKMEHLNNK 480  
QY 481 CKNVVPVYDLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530  
DB 481 CKNVVPVYDLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 4  
AAU27322  
ID AAU27322 standard; protein; 530 AA.  
XX AAU27322;  
XX 18-DEC-2001 (first entry)  
XX Human Oestrogen receptor beta.  
XX Human; Oestrogen receptor beta; ERbeta; SNP; chromosome 6q.25.1;  
KW single nucleotide polymorphism; cardiovascular disease;  
KW autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism;  
KW osteoarthritis; osteoporosis; breast cancer; endometrial cancer.  
XX Homo sapiens.  
XX WO200162793-A2.  
XX 30-AUG-2001.  
XX 20-FEB-2001; 2001WO-US005360.  
XX 22-FEB-2000; 2000US-0183755P.  
XX 24-JAN-2001; 2001US-00768185.  
XX (PEKE ) PE CORP NY.  
XX Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;  
XX WPI; 2001-582041/65.  
XX N-PSDB; AAS43105, AAS43104.  
XX Estrogen receptor gene and protein polymorphisms useful for diagnosis of  
XX individuals at risk of developing bone disorders.  
XX Disclosure; Fig 4; 245pp; English.  
XX The invention relates to a novel isolated peptide comprising or  
XX consisting of an amino acid sequence selected from an amino acid sequence  
XX of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of  
XX 10 amino acids), antibodies against them, nucleic acids encoding them  
XX (including vectors for transforming cells). The gene for human ERbeta is  
XX located on chromosome 6q.25.1. The variants are encoded by single  
XX nucleotide polymorphisms (SNP). The variant peptides and proteins can be  
XX used in assays to determine the biological activity of the protein, to  
XX raise antibodies, as a reagent in assays designed to quantitatively  
XX determine levels of the protein in biological fluids, to identify  
XX compounds that modulate receptor activity and to screen compounds for the  
XX ability to stimulate or inhibit interaction between the receptor protein  
XX and a target molecule that normally interacts with the receptor protein  
XX e.g. oestrogen. The antibody can be used to isolate the protein, to  
XX assess expression in disease states e.g. cardiovascular disease and  
XX autoimmune disease (e.g. systemic lupus erythematosus, arthritis,  
XX rheumatism and osteoarthritis), osteoporosis, breast cancer and  
XX endometrial cancer. In addition the antibodies can be used in  
XX pharmacogenomic analysis and inhibiting protein function, e.g. blocking  
XX the binding of the oestrogen receptor protein to a binding partner such  
XX as a ligand. The nucleic acids encoding the proteins can be used as  
XX probes, primers, chemical intermediates and in biological assays. The  
XX present sequence represents human ERbeta  
XX Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 4; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;  
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNPSLSNPSYNSQSIPLPHGSIYIPSSYVDSHHEYPAWNTYSPAVNYSIPS 60  
 DB 1 MDIKNPSLSNPSYNSQSIPLPHGSIYIPSSYVDSHHEYPAWNTYSPAVNYSIPS 60  
 QY 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYABPQKSPWCEARSLHTLPVN 120  
 DB 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYABPQKSPWCEARSLHTLPVN 120  
 QY 121 RETLKRKVSNGRCASPVTPGSKRDADHFCVCSYASGYHYGVWSCGCKAPFKRSIQGH 180  
 DB 121 RETLKRKVSNGRCASPVTPGSKRDADHFCVCSYASGYHYGVWSCGCKAPFKRSIQGH 180  
 QY 181 NDYICPATNOCTIDKNRKSQACRLKCYEYGVWVKGSRRCRGYRLVRQRSADQLH 240  
 DB 181 NDYICPATNOCTIDKNRKSQACRLKCYEYGVWVKGSRRCRGYRLVRQRSADQLH 240  
 QY 241 CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPFTTEASMMSLTK 300  
 DB 241 CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPFTTEASMMSLTK 300  
 QY 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESQWELMGLMWSIDHPGKLIIFAPDL 360  
 DB 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESQWELMGLMWSIDHPGKLIIFAPDL 360  
 QY 361 VLDRDEGKCVGILEIFDMLLATTSRFRKLQHKYLCVKAMILLNSSMYPLVTATQDA 420  
 DB 361 VLDRDEGKCVGILEIFDMLLATTSRFRKLQHKYLCVKAMILLNSSMYPLVTATQDA 420  
 QY 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSQRMLANLMLLSHVHRASNKGMEHLNLMK 480  
 DB 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSQRMLANLMLLSHVHRASNKGMEHLNLMK 480  
 QY 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530  
 DB 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 5  
 AAE10457  
 ID AAE10457 standard; protein; 530 AA.

AC AAE10457;  
 XX  
 DT 18-DEC-2001 (first entry)

XX Human estrogen receptor (ER)-beta protein.  
 DE  
 XX Estrogen receptor-beta; dietary compound; environmental pollutant;  
 KW red wine; ER-beta mediated cell growth inhibition modulator; human.

XX Homo sapiens.  
 OS

XX WO200169262-A1.  
 PN

XX 20-SEP-2001.  
 PD

XX 15-MAR-2001; 2001WO-US008276.  
 PF

XX 15-MAR-2000; 2000US-0189605P.  
 PR

XX (UYMA-) UNIV MASSACHUSETTS.  
 PA

XX Ho S;  
 PI

XX WPI; 2001-596920/67.  
 DR

XX N-PSDB; AAD18442.  
 DR

XX In vitro screening for modulator of estrogen receptor-beta-mediated cell  
 PT growth inhibition by contacting cell having functional ER-beta protein

PT with candidate compound and detecting ER-beta-regulated gene expression.  
 XX Example 3; Fig 7A; 49pp; English.

CC The invention relates to in vitro screening for modulator of estrogen  
 CC receptor-beta (ER-beta)-mediated cell growth inhibition. The method  
 CC involves contacting mammalian cell having functional ER-beta protein with  
 CC candidate compound and detecting increase/decrease of ER-beta-regulated  
 CC gene expression in presence of candidate compound compared to expression  
 CC in absence of the compound. The method is useful for identifying a  
 CC compound that modulates ER-beta-mediated cell growth inhibition. It is  
 CC useful for testing dietary compounds, e.g. red wine, for the presence of  
 CC estrogen mimics that trigger ER-beta-mediated processes, thus affecting  
 CC physiological function positively or negatively and for testing  
 CC environmental pollutants for the presence of estrogen mimics that may  
 CC pose health risks involving ER-beta-mediated processes. The present  
 CC sequence is human ER-beta protein

XX Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 4; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;  
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNPSLSNPSYNSQSIPLPHGSIYIPSSYVDSHHEYPAWNTYSPAVNYSIPS 60

DB 1 MDIKNPSLSNPSYNSQSIPLPHGSIYIPSSYVDSHHEYPAWNTYSPAVNYSIPS 60

QY 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYABPQKSPWCEARSLHTLPVN 120

DB 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYABPQKSPWCEARSLHTLPVN 120

QY 121 RETLKRKVSNGRCASPVTPGSKRDADHFCVCSYASGYHYGVWSCGCKAPFKRSIQGH 180

DB 121 RETLKRKVSNGRCASPVTPGSKRDADHFCVCSYASGYHYGVWSCGCKAPFKRSIQGH 180

QY 181 NDYICPATNOCTIDKNRKSQACRLKCYEYGVWVKGSRRCRGYRLVRQRSADQLH 240

DB 181 NDYICPATNOCTIDKNRKSQACRLKCYEYGVWVKGSRRCRGYRLVRQRSADQLH 240

QY 241 CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPFTTEASMMSLTK 300

DB 241 CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPFTTEASMMSLTK 300

QY 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESQWELMGLMWSIDHPGKLIIFAPDL 360

DB 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESQWELMGLMWSIDHPGKLIIFAPDL 360

QY 361 VLDRDEGKCVGILEIFDMLLATTSRFRKLQHKYLCVKAMILLNSSMYPLVTATQDA 420

DB 361 VLDRDEGKCVGILEIFDMLLATTSRFRKLQHKYLCVKAMILLNSSMYPLVTATQDA 420

QY 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSQRMLANLMLLSHVHRASNKGMEHLNLMK 480

DB 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSQRMLANLMLLSHVHRASNKGMEHLNLMK 480

QY 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530

DB 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 6

AAE47835

ID AAE47835 standard; protein; 530 AA.

AC AAE47835;

XX 25-MAR-2002 (first entry)

XX Full length estrogen receptor.

XX DNA binding domain; DBD; ligand binding domain; LBD; chimeric receptor;

XX estrogen receptor; ER; chromosome 14; ER-alpha; ER-beta; exon 8;

KW estradiol; nuclear receptor; progesterone receptor.  
 XX Homo sapiens.  
 XX EP1162264-A2.  
 XX 12-DEC-2001.  
 PD 25-MAR-1997; 2001EP-00202021.  
 PF 26-MAR-1996; 96EP-00200820.  
 XX 22-NOV-1996; 96EP-00203284.  
 PR 25-MAR-1997; 97EP-00200903.  
 XX (ALXU) AZZO NOBEL NV.  
 PA Mosselman S, Dijkema R;  
 PI WPI; 2002-084414/12.  
 XX DR N-PSDB; AAL72144.  
 XX New isolated chimeric receptor comprising a DNA binding domain and/or  
 PT ligand binding domain of a new estrogen receptor, for identifying  
 PT functional ligands or hormonal analogs for the receptor.  
 XX Example A; Page 26-28; 35pp; English.  
 PS This sequence shows the full length novel estrogen receptor (ER). The  
 CC additional N-terminal sequences of this sequence, compared to the ER  
 CC sequence given in AAB47834, were generated using RACE PCR. The gene  
 CC encoding this new ER is located on chromosome 14 and has a different  
 CC tissue distribution from classical ER. This ER also has two orphan ER's,  
 CC ER-alpha and ER-beta. These orphan receptors have estrogen receptor  
 CC related structure but do not appear to be able to bind estradiol or other ER  
 CC ligands. The DNA binding domain (DBD) and ligand binding domain (LBD)  
 CC from this ER may be used in the chimeric receptor of the invention which  
 CC also has an N-terminal domain. The chimeric receptor, or DNA encoding it,  
 CC is useful in a screening assay for identification of new drugs. Similar  
 CC chimeric receptors comprising the LBD of the new ER, and also comprising  
 CC the DBD and an N-terminal domain derived from another nuclear receptor  
 CC e.g., progesterone receptor, are useful for the screening of compounds to  
 CC identify new ligands or hormone analogs which are able to activate the  
 CC new ER. Chimeric receptors comprising a DBD of the new ER, and LBD and an  
 CC N-terminal domain derived from another nuclear receptor, can be used to  
 CC identify new ligands or hormone analogs for the nuclear receptors  
 XX Sequence 530 AA;  
 SQ

Query Match 100.0%; Score 2805; DB 5; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;  
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIVIPSSYVDSHHEYPANTFYSPAVMNYSTPS 60  
 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIVIPSSYVDSHHEYPANTFYSPAVMNYSTPS 60  
 61 NVTNLEGGPGRQTTPSNVLPWTFPGHLSPLVVRQLSHLYABPQKSPWCARSLEHTLPVN 120  
 61 NVTNLEGGPGRQTTPSNVLPWTFPGHLSPLVVRQLSHLYABPQKSPWCARSLEHTLPVN 120  
 121 RETLKRKYGNRKASPVTPGSKRDNAHFCVCSYASGYHYGVNSCECKAPKXRSIQGH 180  
 121 RETLKRKYGNRKASPVTPGSKRDNAHFCVCSYASGYHYGVNSCECKAPKXRSIQGH 180  
 181 NDYICPATNOCTIDNRRKSKOACRLKCYEYGVAMVKGSRERCGYRLVRQRSADEQLH 240  
 181 NDYICPATNOCTIDNRRKSKOACRLKCYEYGVAMVKGSRERCGYRLVRQRSADEQLH 240  
 241 CAGKAKRSGHAPRVRELLLDALSPEQLVLTLEAPPHVILSRPSAPFTASMMMSLTK 300  
 241 CAGKAKRSGHAPRVRELLLDALSPEQLVLTLEAPPHVILSRPSAPFTASMMMSLTK 300  
 301 LADKELVHMIWAKKIPGFVELSLFDQVRLLESCHWMEVLMWGLMWSRIDHPGKLIIFAPDL 360

Db 301 LADKELVHMIWAKKIPGFVELSLFDQVRLLESCHWMEVLMWGLMWSRIDHPGKLIIFAPDL 360  
 Qy 361 VLDRDEGKCVGILIEIFDMLLATTSRFRKLQHKSYLCVKAMILLNSSMYPLVATQDA 420  
 Db 361 VLDRDEGKCVGILIEIFDMLLATTSRFRKLQHKSYLCVKAMILLNSSMYPLVATQDA 420  
 Qy 421 DSSRKLHLNAVTDALVWVIAKSGISSQSQSMELANELLMLLSHVRIASNKGMHLLNMK 480  
 Db 421 DSSRKLHLNAVTDALVWVIAKSGISSQSQSMELANELLMLLSHVRIASNKGMHLLNMK 480  
 Qy 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKGSONPQSQ 530  
 Db 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKGSONPQSQ 530

RESULT 7  
 ABG32754  
 ID ABG32754 standard; protein; 530 AA.  
 XX AC ABG32754;  
 DT 15-NOV-2002 (first entry)  
 XX DE Nuclear receptor oestrogen beta (ER beta) protein.  
 XX Human; nuclear receptor oestrogen beta; osteopathic; cytostatic;  
 XX antiarteriosclerotic; neurotropic; neuroprotective; cardiant; cancer;  
 XX osteoporosis; bone disease; reproductive disorder; atherosclerosis;  
 XX cardiovascular disease; Alzheimer's disease.  
 OS Homo sapiens.  
 PN WO200264783-A2.  
 XX 22-AUG-2002.  
 XX 08-FEB-2002; 2002WO-EP001355.  
 PR 09-FEB-2001; 2001EP-00103065.  
 XX 16-MAY-2001; 2001EP-0011862.  
 PA (LION-) LION BIOSCIENCE AG.  
 XX Albers M, Ellwanger S, Loeser E, Koegl M;  
 PI WPI; 2002-643484/69.  
 DR N-PSDB; ABS53304.  
 XX New nucleic acid molecule encoding cofactor (CF) 13, CF14 or CF15 of  
 PT estrogen beta nuclear receptor for treating diseases, e.g. osteoporosis,  
 PT cancer, atherosclerosis or Alzheimer's disease, screening assays and  
 PT scientific research.  
 XX Disclosure; Fig 4; 76pp; English.  
 XX This invention relates to a novel isolated nucleic acid molecule coding  
 CC for a cofactor of the oestrogen beta nuclear receptor. The proteins of  
 CC the invention may have osteopathic, cytostatic, antiarteriosclerotic,  
 CC neurotropic, neuroprotective and cardiant activity. The nucleic acid  
 CC molecule is useful for encoding a cofactor of the oestrogen beta nuclear  
 CC receptor which mediate estrogen receptor transactivation activity and  
 CC thus, provide means for the treatment of numerous diseases such as  
 CC osteoporosis and other bone diseases, failures in reproductive functions,  
 CC cancer, cardiovascular diseases such as atherosclerosis as well as the  
 CC prevention of hot flushes, mood changes and Alzheimer's disease. The  
 CC cofactor proteins are also useful in screening for ligands of the  
 CC oestrogen receptor beta, in screening drugs for agonist and antagonist  
 CC activity, and as scientific research tools, e.g. for developing nucleic  
 CC acid probes or anti-sense oligonucleotides. The proteins may also be used  
 CC for developing antibodies for the detection of these proteins. Methods of  
 CC the invention are useful for developing and identifying compounds for the  
 CC treatment of the above diseases. The present sequence represents the



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CC human oestrogen beta nuclear receptor protein (ER beta) of the invention
XX
SQ Sequence 530 AA;

Query Match      100.0%; Score 2805; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSGYNCSQSIPLHSGSIYIPSSYVDSHHEYPAMTFYSPAVMNSIPS 60
DB 1 MDIKNSPSSLSNPSGYNCSQSIPLHSGSIYIPSSYVDSHHEYPAMTFYSPAVMNSIPS 60

QY 61 NVTNLEGGPGROTTSPNVLPWTPFGHLSPLVHRLSHLYAEPKSPCEARSLHETLPVN 120
DB 61 NVTNLEGGPGROTTSPNVLPWTPFGHLSPLVHRLSHLYAEPKSPCEARSLHETLPVN 120

QY 121 RETLKRKVSNGRNCASPTVTPGSKEDAHFCAVCSDYASGYHGVWSCGCKAFKRSIQGH 180
DB 121 RETLKRKVSNGRNCASPTVTPGSKEDAHFCAVCSDYASGYHGVWSCGCKAFKRSIQGH 180

QY 181 NDYICPATNQCTIDKNRKSQACRLKCYEVGMVKGSRRRCGYRLVRRQRSADQLH 240
DB 181 NDYICPATNQCTIDKNRKSQACRLKCYEVGMVKGSRRRCGYRLVRRQRSADQLH 240

QY 241 CAGKAKRSGGHAPRVRELLLDALSPQVLTLLEAPPHVLIISRPAPPTFASMMNSLTK 300
DB 241 CAGKAKRSGGHAPRVRELLLDALSPQVLTLLEAPPHVLIISRPAPPTFASMMNSLTK 300

QY 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWSRIDHPGKLI FAPDL 360
DB 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWSRIDHPGKLI FAPDL 360

QY 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLQVYKAMILLNSMYPVLTATQDA 420
DB 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLQVYKAMILLNSMYPVLTATQDA 420

QY 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLSHVHRHASKGMEHLNWK 480
DB 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLSHVHRHASKGMEHLNWK 480

QY 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
DB 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 8
ADA83824
ID ADA83824 standard; protein; 530 AA.
XX
AC ADA83824;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human ESR2 protein.
XX
KW human; marker; expressed sequence tag; EST; arabisidopsis; tumour;
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW vaccine.
XX
OS Homo sapiens.
XX
PN W02002103028-A2.
XX
FD 27-DEC-2002.
XX
PF 30-MAY-2002; 2002MO-1B004189.
XX
PR 30-MAY-2001; 2003US-0293999P.
XX
PR 22-OCT-2001; 2001US-0330457P.
XX
PR 19-FEB-2002; 2002US-0357144P.
XX
XX (BIOM-) BIOMEDICAL CENT.
XX

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PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LI;
XX WPI: 2003-175241/17.
DR N-PSDB; AD83823.
XX
PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 29; Page 217-220; 516pp; English.
XX
XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.
XX
SQ Sequence 530 AA;

Query Match      100.0%; Score 2805; DB 6; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSGYNCSQSIPLHSGSIYIPSSYVDSHHEYPAMTFYSPAVMNSIPS 60
DB 1 MDIKNSPSSLSNPSGYNCSQSIPLHSGSIYIPSSYVDSHHEYPAMTFYSPAVMNSIPS 60

QY 61 NVTNLEGGPGROTTSPNVLPWTPFGHLSPLVHRLSHLYAEPKSPCEARSLHETLPVN 120
DB 61 NVTNLEGGPGROTTSPNVLPWTPFGHLSPLVHRLSHLYAEPKSPCEARSLHETLPVN 120

QY 121 RETLKRKVSNGRNCASPTVTPGSKEDAHFCAVCSDYASGYHGVWSCGCKAFKRSIQGH 180
DB 121 RETLKRKVSNGRNCASPTVTPGSKEDAHFCAVCSDYASGYHGVWSCGCKAFKRSIQGH 180

QY 181 NDYICPATNQCTIDKNRKSQACRLKCYEVGMVKGSRRRCGYRLVRRQRSADQLH 240
DB 181 NDYICPATNQCTIDKNRKSQACRLKCYEVGMVKGSRRRCGYRLVRRQRSADQLH 240

QY 241 CAGKAKRSGGHAPRVRELLLDALSPQVLTLLEAPPHVLIISRPAPPTFASMMNSLTK 300
DB 241 CAGKAKRSGGHAPRVRELLLDALSPQVLTLLEAPPHVLIISRPAPPTFASMMNSLTK 300

QY 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWSRIDHPGKLI FAPDL 360
DB 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWSRIDHPGKLI FAPDL 360

QY 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLQVYKAMILLNSMYPVLTATQDA 420
DB 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLQVYKAMILLNSMYPVLTATQDA 420

QY 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLSHVHRHASKGMEHLNWK 480
DB 421 DSSRKLHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLSHVHRHASKGMEHLNWK 480

QY 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
DB 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

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CC amount of the receptor monomer and the amount of the receptor/test  
 CC substance/nucleic acid fragment complex with relative values. The nucleic  
 CC acid is DNA. The detection is carried out according to high-throughput  
 CC detection. The present sequence represents human oestrogen receptor beta  
 CC (hERbeta) which is coupled to green fluorescent protein (GFP) and used in  
 CC the method of the invention  
 XX  
 XX Sequence 530 AA;  
 SQ

Query Match 100.0%; Score 2805; DB 7; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;  
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLSNPSYNCSSILPLEHSGSYIIPSSYVDSHHEYPAMFYSPAVNNYSIPS 60  
 Db 1 MDIKNSPSSLSNPSYNCSSILPLEHSGSYIIPSSYVDSHHEYPAMFYSPAVNNYSIPS 60

Qy 61 NVTNLEGGPGRTTSPNVLWFTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLHTLPVN 120  
 Db 61 NVTNLEGGPGRTTSPNVLWFTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLHTLPVN 120

Qy 121 RETLKRKVSNGRCASPVTPGSGKDDAHPCAVCSDYASGYHYGVWSCGCKAFKYSIQGH 180  
 Db 121 RETLKRKVSNGRCASPVTPGSGKDDAHPCAVCSDYASGYHYGVWSCGCKAFKYSIQGH 180

Qy 181 NDYICPATNCTIDKNRKKSCQACRLKCYEVGMVKGSRRCRGYRLVRRQSADEQLH 240  
 Db 181 NDYICPATNCTIDKNRKKSCQACRLKCYEVGMVKGSRRCRGYRLVRRQSADEQLH 240

Qy 241 CAGKAKSGGHAHPVRRELLLDALSPQLVTLLEAPPHVLIISPPSAPPTFASMMMSLTK 300  
 Db 241 CAGKAKSGGHAHPVRRELLLDALSPQLVTLLEAPPHVLIISPPSAPPTFASMMMSLTK 300

Qy 301 LADKELVHMLSWAKKIGFVELSLFDQVRLLESCEMVEMLMGLMWRSIDHPGKLIIFAPDL 360  
 Db 301 LADKELVHMLSWAKKIGFVELSLFDQVRLLESCEMVEMLMGLMWRSIDHPGKLIIFAPDL 360

Qy 361 VLDRECKCVEGILEIFDMLLATTFRRELKQHKYLCVKAMILLNSSMYPVLTATODA 420  
 Db 361 VLDRECKCVEGILEIFDMLLATTFRRELKQHKYLCVKAMILLNSSMYPVLTATODA 420

Qy 421 DSSRKLHLLNAVTDALVWVIKSGISSQOOSMELANILLSHVHRASNKGMEHLLNMK 480  
 Db 421 DSSRKLHLLNAVTDALVWVIKSGISSQOOSMELANILLSHVHRASNKGMEHLLNMK 480

Qy 481 CKNVVPVYDILLENLNAHVLGRCKSSITGSECPAEDSKSKEGSONPQSQ 530  
 Db 481 CKNVVPVYDILLENLNAHVLGRCKSSITGSECPAEDSKSKEGSONPQSQ 530

RESULT 10  
 ADE12138  
 ID ADE12138 standard; protein; 530 AA.  
 XX  
 AC ADE12138;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human oestrogen receptor beta.  
 XX  
 KW Human; oestrogen receptor beta;  
 KW oestrogen-dependent genitourinary condition; leiomyoma; fibroid;  
 KW pregnancy prevention; gynaecological; cytostatic; contraceptive;  
 KW receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003199472-A1.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 19-MAR-2003; 2003US-00192274.  
 XX

RESULT 9  
 ABU61628  
 ID ABU61628 standard; protein; 530 AA.  
 XX  
 AC ABU61628;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Human oestrogen receptor beta, hERbeta.  
 XX  
 KW Human; oestrogen receptor beta; hER beta; receptor; FCS; FIDA;  
 KW fluorescence correlation spectroscopy; green fluorescent protein; GFP;  
 KW fluorescence intensity distribution analysis; nuclear receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003022224-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 19-JUL-2002; 2002US-00198785.  
 XX  
 PR 19-JUL-2001; 2001JP-00220444.  
 PR 23-JUL-2001; 2001JP-00221963.  
 XX  
 PA (OLYU) OLYMPUS OPTICAL CO LTD.  
 XX  
 PI Sakamoto H, Kato N, Okamoto N;  
 XX  
 DR WPI; 2003-479487/45.  
 DR N-PSDB; AC61448.  
 XX  
 PT Detecting binding capacity of test substance, with respect to a protein,  
 PT by reacting test substance with fluorescence-labeled protein and  
 PT detecting change in the fluorescence intensity.  
 XX  
 PS Disclosure; Page 18-19; 30pp; English.  
 XX

The invention relates to detecting the presence/absence of binding  
 CC capacity of a test substance, with respect to a protein, involves having  
 CC a protein, which has been labeled with fluorescence material, exist in a  
 CC solution and while successively measuring fluorescence intensity from the  
 CC fluorescent material, reacting the test substance with labeled protein  
 CC and determining binding capacity of the test substance, with respect to  
 CC protein, on basis of successive change in fluorescent intensity. Also  
 CC included is producing a protein which has been labeled with fluorescence,  
 CC involving construction an expression vector by incorporating a gene  
 CC encoding the protein, a gene encoding a fluorescent material for labeling  
 CC the protein, and a promoter for expressing in vitro the gene encoding the  
 CC protein, and having the expression vector exist in a solution which  
 CC allows expression and transcription of the genes and production of the  
 CC protein, thus producing the protein labeled with the fluorescent  
 CC material. The protein is a hormone receptor (e.g. an oestrogen receptor),  
 CC antigen or antibody. The method is useful for detecting a binding  
 CC reaction of a test substance to a receptor, by maintaining a receptor  
 CC (which has been labeled with a marker material capable of generating a  
 CC light signal), a test substance, and a nucleic acid fragment having a  
 CC specific nucleic acid sequence which allows binding of a receptor/ligand  
 CC complex to it, in a solution in which the receptor and the ligand can  
 CC form a complex and this receptor/ligand complex can be bound to the  
 CC specific nucleic acid sequence, and detecting the presence/absence of the  
 CC complex. The presence/absence of the receptor/test substance/nucleic acid  
 CC fragment complex is detected by measuring diffusion time, in the  
 CC solution, of the labeled receptor. The measurement is performed by  
 CC fluorescence correlation spectroscopy (FCS) or fluorescence intensity  
 CC distribution analysis (FIDA). The receptor is a nuclear receptor. The  
 CC nucleic acid fragment having the specific nucleic acid sequence has  
 CC molecular weight which is not smaller than that of the receptor, and a  
 CC diffusion constant which is not larger than that of the receptor. Binding  
 CC affinity of the test substance with respect to the receptor is evaluated  
 CC by expressing, through calculation using an autocorrelation function, the

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PR 19-MAR-2002; 2002US-0365760P.
XX (TEXA ) UNIV TEXAS SYSTM.
PA (NOUN ) UNIV NORTHWESTERN.
XX
XX AI-Hendy A, Lee EJ, Jameson JL;
XX PI
XX WPI; 2003-852811/79.
DR N-PSDB; ADE12137.
XX
XX Treating an estrogen-dependent genitourinary condition in a patient by
PT administering to the patient an expression construct comprising a nucleic
PT acid sequence encoding a modified estrogen receptor e.g., leiomyoma or
PT fibroid.
XX
XX Claim 27; SEQ ID NO 4; 459p; English.
XX
XX The invention relates to a method for treating an oestrogen-dependent
CC genitourinary condition in a patient comprising administering an
CC expression construct comprising a nucleic acid sequence encoding a
CC modified oestrogen receptor. The sequence is under the control of a
CC promoter. The method is useful for treating an oestrogen-dependent
CC genitourinary condition in a patient, e.g., leiomyoma or fibroids, or for
CC preventing pregnancy. This sequence represents the human oestrogen
CC receptor beta polypeptide of the invention.
XX
XX Sequence 530 AA;
XX
Query Match 100.0%; Score 2805; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 60
DB 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 60
QY 61 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRQLSHLYABPQKSPWCARSLEHTLPVN 120
DB 61 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRQLSHLYABPQKSPWCARSLEHTLPVN 120
QY 121 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYDASGYHYGWSCEGCKAFPKRSIQGH 180
DB 121 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYDASGYHYGWSCEGCKAFPKRSIQGH 180
QY 181 NDYICPATNQCTIDKNRKSQAACRLRKCYEVGMVKCGRRRCGYRLVVRORSADQLH 240
DB 181 NDYICPATNQCTIDKNRKSQAACRLRKCYEVGMVKCGRRRCGYRLVVRORSADQLH 240
QY 241 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLTLSRPSAPFTASMMSLTK 300
DB 241 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLTLSRPSAPFTASMMSLTK 300
QY 301 LADKELVHMTISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDPL 360
DB 301 LADKELVHMTISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDPL 360
QY 361 VLDRDGKCVGELIETPDMLATTSRFRELKLOHKEYLVCVKAMILLNSNYPVLTATQDA 420
DB 361 VLDRDGKCVGELIETPDMLATTSRFRELKLOHKEYLVCVKAMILLNSNYPVLTATQDA 420
QY 421 DSSRKLHLNLNAVTDALVWYIAKSGISSQQQSMRLANLLMLLSVHRASNKGMHLLNKK 480
DB 421 DSSRKLHLNLNAVTDALVWYIAKSGISSQQQSMRLANLLMLLSVHRASNKGMHLLNKK 480
QY 481 CRNVWPVYDILLEIMAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
DB 481 CRNVWPVYDILLEIMAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

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RESULT 11
AY07270
ID AAY07270 standard; protein; 548 AA.
XX

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AC AAY07270;
XX 06-JUL-1999 (first entry)
XX Human oestrogen receptor.
XX
XX Human; oestrogen receptor; ligand; bone resorption; metabolic disorder;
XX cardiovascular disease; cancer; central nervous system; breast; uterine;
XX osteoporosis; ovarian; prostate; diabetes; Alzheimer's disease.
XX
XX Homo sapiens.
XX WO9912961-A1.
XX 18-MAR-1999.
XX
XX 04-SEP-1998; 98WO-US018577.
XX
XX 08-SEP-1997; 97US-0058271P.
XX 30-SEP-1997; 97US-0060520P.
XX 30-OCT-1997; 97GB-00022884.
XX 20-MAR-1998; 98GB-00006032.
XX (MERI ) MERCK & CO INC.
XX Wilkinson H;
XX
XX WPI; 1999-229222/19.
XX N-PSDB; AAX34309.
XX
XX Estrogen receptor useful in ligand identification in medicine.
XX
XX Claim 1; Fig 1; 32pp; English.
XX
XX This sequence represents a human oestrogen receptor. The receptor can be
XX used to identify ligands that bind to human oestrogen receptor. The
XX ligands can be used in a method for preventing or treating an oestrogen
XX receptor mediated disease or condition, such as abnormal bone resorption,
XX a cardiovascular disease, cancer, metabolic disorders, or central nervous
XX system disorders. The ligand is especially used to treat osteoporosis,
XX breast, uterine, ovarian or prostate cancer, diabetes or Alzheimer's
XX disease
XX
XX Sequence 548 AA;
XX
Query Match 100.0%; Score 2805; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.5e-258;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 60
DB 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 78
QY 61 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRQLSHLYABPQKSPWCARSLEHTLPVN 120
DB 79 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRQLSHLYABPQKSPWCARSLEHTLPVN 138
QY 121 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYDASGYHYGWSCEGCKAFPKRSIQGH 180
DB 139 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYDASGYHYGWSCEGCKAFPKRSIQGH 198
QY 181 NDYICPATNQCTIDKNRKSQAACRLRKCYEVGMVKCGRRRCGYRLVVRORSADQLH 240
DB 199 NDYICPATNQCTIDKNRKSQAACRLRKCYEVGMVKCGRRRCGYRLVVRORSADQLH 258
QY 241 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLTLSRPSAPFTASMMSLTK 300
DB 259 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLTLSRPSAPFTASMMSLTK 318
QY 301 LADKELVHMTISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDPL 360
DB 319 LADKELVHMTISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDPL 378

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QY 361 VLDRDEGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCKVAMILLNSSMYPLVTATQDA 420  
 DB 379 VLDRDEGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCKVAMILLNSSMYPLVTATQDA 438  
 QY 421 DSSRKLHLNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRHASKNGHEHLNWK 480  
 DB 439 DSSRKLHLNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRHASKNGHEHLNWK 498  
 QY 481 CKNVVPYDILLEMLNAFVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530  
 DB 499 CKNVVPYDILLEMLNAFVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 548

## RESULT 12

ABB80756  
 ID ABB80756 standard; protein; 793 AA.

XX AC ABB80756;

XX DT 23-SEP-2002 (first entry)

XX DE Amino acid sequence of a fusion GFP/HER beta protein.

XX KW Fluorometric analyzer; laser; fluorescence; GFP; ER beta; human; gene;  
 green fluorescent protein; estrogen receptor beta; fusion protein.

XX OS Synthetic.

XX OS Aequorea victoria.

XX OS Homo sapiens.

XX PN W0200248693-A1.

XX PX 20-JUN-2002.

XX PF 14-DEC-2001; 2001WO-JP010998.

XX PR 14-DEC-2000; 2000JP-00380327.

XX PR 30-JAN-2001; 2001JP-00022105.

XX PA (OLYU) OLYMPUS OPTICAL CO LTD.

XX PI Kato N, Sakamoto H;

XX DR WPI; 2002-528176/56.

XX DR N-PSDB; ABN86125.

XX PT Autocorrection function-embedded confocal optics-based fluorometric  
 analyzers for studying behaviors of fluorescence-labeled molecules  
 particularly intracellular biological molecules like proteins at  
 molecular level.

XX PS Example 2; Page 98-105; 109pp; Japanese.

XX CC The invention relates to a fluorometric analyzer that comprises a laser  
 light source, an optical system for focusing the light beam from laser  
 light source to a sample to form a confocal region, another optical  
 system for focusing fluorescence from the sample, a light detector for  
 measuring intensity, and a recording means to record the variation of  
 intensity in the measured fluorescence. The analyzers are for studying  
 behaviors of fluorescence-labeled molecules particularly intracellular  
 biological molecules like proteins at molecular level, e.g. protein  
 functions and interactions. Such analyzers are stable and convenient to  
 operate, thereby enabling easy performance of fluorescence correlation  
 spectroscopy, fluorescence intensity distribution analysis and  
 fluorescence intensity multiple distribution analysis. The present  
 sequence represents the amino acid sequence of a fusion protein  
 comprising a GFP (green fluorescent protein) and hER (human estrogen  
 receptor) beta protein

XX SQ Sequence 793 AA;

Query Match 100.0%; Score 2805; DB 5; Length 793;

Best Local Similarity 100.0%; Pred. No. 4,4e-258;

	Matches	530;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MDIKNSPSSINPSSNCSQSIPLPHEGSIYIPSSVDSHHEYPAMTFSPAMNTSIPS	60							
DB	264	MDIKNSPSSINPSSNCSQSIPLPHEGSIYIPSSVDSHHEYPAMTFSPAMNTSIPS	323							
QY	61	NVTNLEGGPGROTTSPNVLPWTPGHLSPVWVHQLSHLYAEPKSPWCSEARSLEHTLPVN	120							
DB	324	NVTNLEGGPGROTTSPNVLPWTPGHLSPVWVHQLSHLYAEPKSPWCSEARSLEHTLPVN	383							
QY	121	RETLKEKVSNGRCASPVTPGSKRDAHFCAVCSDYASGVHYGWSCEGCKAFPKRSIQGH	180							
DB	384	RETLKEKVSNGRCASPVTPGSKRDAHFCAVCSDYASGVHYGWSCEGCKAFPKRSIQGH	443							
QY	181	NDYICPATNQCTIDKRRKSCQACRLKCYEVGKVGWKGSRRCRGYLVRRQRSADEQLH	240							
DB	444	NDYICPATNQCTIDKRRKSCQACRLKCYEVGKVGWKGSRRCRGYLVRRQRSADEQLH	503							
QY	241	CAGKAKRSGGHAPRVRELLLDALSPQQLVLTLEAEPHPHVLISRPSPAPFTEASMMSLTK	300							
DB	504	CAGKAKRSGGHAPRVRELLLDALSPQQLVLTLEAEPHPHVLISRPSPAPFTEASMMSLTK	563							
QY	301	LADKELVHMISNAKKIPGFVELSLPDQVRLBSCWMEVLMGLMWSIDHPGKLIAPDDL	360							
DB	564	LADKELVHMISNAKKIPGFVELSLPDQVRLBSCWMEVLMGLMWSIDHPGKLIAPDDL	623							
QY	361	VLDRDEGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCKVAMILLNSSMYPLVTATQDA	420							
DB	624	VLDRDEGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCKVAMILLNSSMYPLVTATQDA	683							
QY	421	DSSRKLHLNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRHASKNGHEHLNWK	480							
DB	684	DSSRKLHLNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRHASKNGHEHLNWK	743							
QY	481	CKNVVPYDILLEMLNAFVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ	530							
DB	744	CKNVVPYDILLEMLNAFVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ	793							

## RESULT 13

AAW14724

ID AAW14724 standard; protein; 485 AA.

XX AC AAW14724;

XX DT 08-JUN-1997 (first entry)

XX DE Human oestrogen receptor beta (ER-beta).

XX KW Orphan receptor; oestrogen receptor beta; ER-beta; nuclear receptor;  
 prostate cancer; benign prostatic hyperplasia; ovary cancer;  
 cardiovascular disease; osteoporosis; environment; pollutant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 104..169

XX FT Domain /label=DNA-binding\_domain

XX FT Domain 260..457

XX FT Domain /label=Ligand-binding\_domain

XX PN W09709348-A2.

XX PD 13-MAR-1997.

XX PF 09-SEP-1996; 96WO-EP003933.

XX PR 08-SEP-1995; 95GE-00018272.

XX PR 15-MAR-1996; 96GE-00005550.

XX PR 11-APR-1996; 96GE-00007532.

XX PR 08-MAY-1996; 96GE-00009576.

XX PA (KARO-) KARO BIO AB.

XX PI Kuiper GG, Emark E, Gustafsson J;  
 XX DR WPI: 1997-192842/17.  
 XX DR N-PSDB; AAT62843.  
 XX PT New isolated oestrogen receptor beta - used to develop prods. for  
 XX PT treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular  
 XX PT disease.  
 XX PS Claim 1; Fig 13A; 45pp; English.  
 XX CC A novel human orphan receptor (AAW14724) is related to the known  
 CC oestrogen receptor ER-alpha, and has been designated ER-beta. It is an  
 CC oestrogen receptor-related nuclear receptor. The ER-beta amino acid  
 CC sequence was deduced from a cDNA clone (AAT62843) isolated from a human  
 CC testis cDNA library. Rat, human and mouse ER-beta (AAW14723-25) can be  
 CC used to isolate molecules for use in the treatment of cardiovascular  
 CC diseases, central nervous system diseases, osteoporosis, prostate or  
 CC ovarian cancer or benign prostatic hyperplasia and to test environmental  
 CC chemicals for oestrogenic activity  
 XX SQ Sequence 485 AA;  
 Query Match 91.1%; Score 2554; DB 2; Length 485;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234; Mismatches 1; Indels 0; Gaps 0;  
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 46 MTFTSPAVNYSIPSNVTNLEGGPGRQTTPNVLMPPTGHLSPVLVHRLSHLYAEPK 105  
 DB 1 MTFTSPAVNYSIPSNVTNLEGGPGRQTTPNVLMPPTGHLSPVLVHRLSHLYAEPK 60  
 QY 106 PWCEARSLEHTLPVNRRETLKRVSGNRCASPTVGSKEDAHFCAVCSYASGYHYGWS 165  
 DB 61 PWCEARSLEHTLPVNRRETLKRVSGNRCASPTVGSKEDAHFCAVCSYASGYHYGWS 120  
 QY 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEYGVGKCGSRRCG 225  
 DB 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEYGVGKCGSRRCG 180  
 QY 226 YRLVRRQRSADQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLLAEPPHVLISRP 285  
 DB 181 YRLVRRQRSADQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLLAEPPHVLISRP 240  
 QY 286 SAPFTASMMSLTKLADKELVHMSWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 345  
 DB 241 SAPFTASMMSLTKLADKELVHMSWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 300  
 QY 346 RSIDHPGKLI FAPDLVLDREDEKCVGEILEIFDMLLATTSSRFRELKQHEYLVCVAMIL 360  
 DB 301 RSIDHPGKLI FAPDLVLDREDEKCVGEILEIFDMLLATTSSRFRELKQHEYLVCVAMIL 360  
 QY 406 LNSSMYPLVTATQDADSSRLKLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLSHV 465  
 DB 361 LNSSMYPLVTATQDADSSRLKLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLSHV 420  
 QY 466 RHASNKGMEHLLNKKCNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQ 525  
 DB 421 RHASNKGMEHLLNKKCNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQ 480  
 QY 526 NPQSQ 530  
 DB 481 NPQSQ 485

RESULT 14

AAY01597

ID AAY01597 standard; protein; 485 AA.

XX AC

XX AC AAY01597;

XX DT

17-JUN-1999 (first entry)

XX

DE An estrogen receptor-beta protein.  
 XX differential estrogen receptor; ER-alpha; ER-beta; activation; API site;  
 KW therapy.  
 XX Homo sapiens.  
 OS W0911760-A1.  
 XX 11-MAR-1999.  
 PD 31-AUG-1998; 98WO-US018030.  
 XX 04-SEP-1997; 97US-00923708.  
 XX (REGC) UNIV CALIFORNIA.  
 XX Kushner FJ, Gustafsson J, Kuiper GGJM, Nilsson S, Paech K;  
 PI Scanlan TS, Webb P;  
 XX WPI: 1999-205173/17.  
 DR N-PSDB; AAX26686.  
 XX Screening for test compounds which inhibit or activate estrogen receptor  
 PT beta (ER-beta) mediated activation at a API site - for use in therapy.  
 PT Claim 14; Page 43-44; 61pp; English.  
 PS The present sequence represents an estrogen receptor-beta. The  
 XX specification describes a method for screening test compounds for  
 CC differential estrogen receptor (ER) alpha-mediated and ER beta-mediated  
 CC activation at an API site. The method is used for identifying compounds  
 CC which can be used in therapy  
 XX SQ Sequence 485 AA;  
 Query Match 90.4%; Score 2535; DB 2; Length 485;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-232; Mismatches 4; Indels 0; Gaps 0;  
 Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 46 MTFTSPAVNYSIPSNVTNLEGGPGRQTTPNVLMPPTGHLSPVLVHRLSHLYAEPK 105  
 DB 1 MTFTSPAVNYSIPSNVTNLEGGPGRQTTPNVLMPPTGHLSPVLVHRLSHLYAEPK 60  
 QY 106 PWCEARSLEHTLPVNRRETLKRVSGNRCASPTVGSKEDAHFCAVCSYASGYHYGWS 165  
 DB 61 PWCEARSLEHTLPVNRRETLKRVSGNRCASPTVGSKEDAHFCAVCSYASGYHYGWS 120  
 QY 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEYGVGKCGSRRCG 225  
 DB 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACRLKCYEYGVGKCGSRRCG 180  
 QY 226 YELVRRQRSADQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLLAEPPHVLISRP 285  
 DB 181 YELVRRQRSADQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLLAEPPHVLISRP 240  
 QY 286 SAPFTASMMSLTKLADKELVHMSWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 345  
 DB 241 SAPFTASMMSLTKLADKELVHMSWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 300  
 QY 346 RSIDHPGKLI FAPDLVLDREDEKCVGEILEIFDMLLATTSSRFRELKQHEYLVCVAMIL 405  
 DB 301 RSIDHPGKLI FAPDLVLDREDEKCVGEILEIFDMLLATTSSRFRELKQHEYLVCVAMIL 360  
 QY 406 LNSSMYPLVTATQDADSSRLKLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLSHV 465  
 DB 361 LNSSMYPLVTATQDADSSRLKLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLSHV 420  
 QY 466 RHASNKGMEHLLNKKCNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQ 525  
 DB 421 RHASNKGMEHLLNKKCNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGQ 480  
 QY 526 NPQSQ 530

QY 354 LIFAPDLVDRDEGKCVGILEIFDMLLATTSRRELKLOHKEYLCVKAMILLNSSMYPL 413  
Db 301 LIFAPDLVDRDEGKCVGILEIFDMLLATTSRRELKLOHKEYLCVKAMILLNSSMYPL 360  
QY 414 VTATODADSSRKLALHLLNAVTDALVWVIKSGISSQSSMRLANLMLLSHVRHASKGM 473  
Db 361 VTATODADSSRKLALHLLNAVTDALVWVIKSGISSQSSMRLANLMLLSHVRHASKGM 420  
QY 474 EHLNKKCNVVPVYDILLEMLNAHVLRGCKSSITGSECPAEDSKSKGSONPQSQ 530  
Db 421 EHLNKKCNVVPVYDILLEMLNAHVLRGCKSSITGSECPAEDSKSKGSONPQSQ 477

Search completed: June 20, 2004, 10:37:11  
Job time : 62 secs

Db 481 NLQSQ 485  
RESULT 15  
AAW33212  
ID AAW33212 standard; protein; 477 AA.  
XX AC  
XX AAW33212;  
DT 20-APR-1998 (first entry)  
XX DE Human oestrogen receptor protein.  
XX KW Oestrogen receptor protein; steroid; alternative splicing; estradiol;  
XX KW estone; estriol; screening.  
XX OS Homo sapiens.  
XX PN EP798378-A2.  
XX PD 01-OCT-1997.  
XX PF 25-MAR-1997; 97EP-00200903.  
XX PR 26-MAR-1996; 96EP-00200820.  
XX PR 22-NOV-1996; 96EP-00203284.  
XX PA (ALKU ) AKZO NOBEL NV.  
XX PI Mosselman S, Dijkema R;  
XX DR WPI; 1997-473188/44.  
XX DR N-PSDB; AAT88412.  
XX PT DNA encoding estrogen receptor - useful in screening assay to identify  
XX PT novel ligands or hormonal analogues.  
XX PS Claim 4; Page 18-20; 45pp; English.  
XX CC This sequence represents a novel oestrogen binding protein. The cDNA  
XX CC sequence which encodes this protein can be alternatively spliced  
XX CC resulting in the detection of additional transcripts (see AAT88413). This  
XX CC receptor is able to bind and be activated by estradiol, estone and  
XX CC estriol, can be used in a screening assay for the identification of new  
XX CC drugs e.g. novel ligands or hormonal analogues  
XX SQ Sequence 477 AA;  
Query Match 89.9%; Score 2522; DB 2; Length 477;  
Best Local Similarity 100.0%; Pred. No. 2.1e-231; Indels 0; Gaps 0;  
Matches 477; Conservative 0; Mismatches 0;  
QY 54 MNYISIPNVTNLEGPGRQTTPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEARSL 113  
Db 1 MNYISIPNVTNLEGPGRQTTPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEARSL 60  
QY 114 EHTLPVNRETLKRKVSNGRCASPTGPGSKDAHFCAVCSDYASGVHYGWSCEGCKAPP 173  
Db 61 EHTLPVNRETLKRKVSNGRCASPTGPGSKDAHFCAVCSDYASGVHYGWSCEGCKAPP 120  
QY 174 KRSIQGHNDYICPATNCTIDKNRKSQACRLKCYEVMKCGRRRCGYRLVRQR 233  
Db 121 KRSIQGHNDYICPATNCTIDKNRKSQACRLKCYEVMKCGRRRCGYRLVRQR 180  
QY 234 SADEQLHCAGKAKSGGHPVRILLDLSPQLVLTLEAPPVHLISRPSAPFEAS 293  
Db 181 SADEQLHCAGKAKSGGHPVRILLDLSPQLVLTLEAPPVHLISRPSAPFEAS 240  
QY 294 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSIDHPGX 353  
Db 241 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSIDHPGX 300

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:35:07 ; Search time 21 Seconds  
(without alignments)  
2427.691 Million cell updates/sec

Title: US-08-906-365-2  
Perfect score: 2805  
Sequence: 1 MDIKNSPSSNSPSSVNCQ.....ECSPAEDSKSKEGQNPOSQ 530

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 78: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2805	100.0	530	2 JCS939	estrogen receptor
2	2522	89.9	477	2 S71400	estrogen receptor
3	2284	81.4	503	2 JW0046	estrogen receptor
4	1230.5	43.9	589	1 QRCHE	estrogen receptor
5	1224.5	43.7	595	1 QRHUE	estrogen receptor
6	1219.5	43.5	595	2 I47140	estrogen receptor
7	1218.5	43.4	599	1 ORKSE	estrogen receptor
8	1216.5	43.4	600	1 ORKTE	estrogen receptor
9	1214	43.3	586	1 QRLXE	estrogen receptor
10	1199	42.7	620	2 T10423	estrogen receptor
11	1174.5	41.9	701	2 S64737	80K estrogen recep
12	1134.5	40.4	535	2 S58224	estrogen receptor
13	1120	39.9	574	2 A37197	estrogen receptor
14	631.5	22.5	433	2 B29345	steroid hormone re
15	619.5	22.1	433	2 S58087	estrogen receptor
16	597.5	21.3	521	2 A43345	steroid hormone re
17	471	16.8	467	2 A43781	retinoid-X-recepto
18	469.5	16.7	923	2 A39596	progesterone recep
19	465	16.6	923	2 I53280	progesterone recep
20	459	16.4	446	2 A34418	H-2 region II bind
21	459	16.4	451	2 A41651	retinoic acid rece
22	458.5	16.3	533	2 S37781	retinoid X recepto
23	457.5	16.3	758	2 S60586	glucocorticoid rec
24	456	16.3	448	2 D41727	retinoid X recepto
25	456	16.3	520	2 I84718	RXR-beta1 isoform
26	455.5	16.2	410	2 S28669	retinoic acid rece
27	453	16.1	948	2 JG0194	androgen receptor
28	453	16.1	930	2 A25923	progesterone recep
29	452	16.1	463	2 S26670	retinoic acid rece

## RESULT 1

JCS939

estrogen receptor beta - human

C:Species: Homo sapiens (man)

C>Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000

C:Accession: JCS939

R:Ogawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Murai

Biochem. Biophys. Res. Commun. 243, 122-126, 1998

A:Title: The complete primary structure of human estrogen receptor beta (hERbeta) and

A:Reference number: JCS939; MUID:98139878; PMID:9473491

A:Accession: JCS939

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1530 <OGA>

A:Cross-references: DDBJ:AB06590; NID:G2911151; PID:BA24953.1; PID:G2911152

A:Superfamily: estrogen receptor; erba transforming protein Homology

F:147-408/Domain: erba transforming protein homology <ERB>

Query Match 100.0%; Score 2805; DB 2; Length 530;

Best Local Similarity 100.0%; Pred. No. 7.3e-211;

Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDIKNSPSSNSPSSVNCQSLPLEHGSIVTPSSVNSHHEYPAMTVPSPAMVNSIPS	60
DB	1	MDIKNSPSSNSPSSVNCQSLPLEHGSIVTPSSVNSHHEYPAMTVPSPAMVNSIPS	60
QY	61	NVTNLEGGPGRTTSPNVLPWTPGHLSPVWHRQLSHLYAEPQKPCWCEASLEHTLPVN	120
DB	61	NVTNLEGGPGRTTSPNVLPWTPGHLSPVWHRQLSHLYAEPQKPCWCEASLEHTLPVN	120
QY	121	RETLKXKUSGNCCASPVTPGSGKRDHFCVCSDVASGVHYGVNSCEGCKAFKESIQH	180
DB	121	RETLKXKUSGNCCASPVTPGSGKRDHFCVCSDVASGVHYGVNSCEGCKAFKESIQH	180
QY	181	NDYICPATNQCTIDKNRRKSCOACLRKYGVGMVKGSRRCGRLVRRQSRSADEQLH	240
DB	181	NDYICPATNQCTIDKNRRKSCOACLRKYGVGMVKGSRRCGRLVRRQSRSADEQLH	240
QY	241	CAGKARSGGHPRVRELLLDALSPQLVLTLEAPPHVLISRPSPAPPTASMMMSITK	300
DB	241	CAGKARSGGHPRVRELLLDALSPQLVLTLEAPPHVLISRPSPAPPTASMMMSITK	300
QY	301	LADKELVHMSWAKKIPGVFVLSLFDQVRLLESCHMEVLMGLMWRSIDHPGKLIIFAPDL	360
DB	301	LADKELVHMSWAKKIPGVFVLSLFDQVRLLESCHMEVLMGLMWRSIDHPGKLIIFAPDL	360
QY	361	VDROEGKVEGILAIIDMLLATSFRRELKLOHKEYLCVKAMILLNSMPLVATQDA	420
DB	361	VDROEGKVEGILAIIDMLLATSFRRELKLOHKEYLCVKAMILLNSMPLVATQDA	420
QY	421	DSSRLAHLNAVTDALVWVIAKSGISSQQSMRLANILLSHVHRHASNKGMEHLNKK	480
DB	421	DSSRLAHLNAVTDALVWVIAKSGISSQQSMRLANILLSHVHRHASNKGMEHLNKK	480

## ALIGNMENTS

Db 421 DSRKLAHLNNAVTDALVWVIAKSGISSQQSMRLANLLMLLSHVHRASNKGMEHLNWK 480

Qy 481 CKNVVPPYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSKGSONPQSQ 530

Db 481 CKNVVPPYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSKGSONPQSQ 530

RESULT 2

S71400

estrogen receptor beta - human

C:Species: Homo sapiens (man)

C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 20-Jun-2000

C:Accession: S71400

R:Mooselman, S.; Poelman, J.; Dijkema, R.

FEBS Lett. 392, 49-53, 1996

A:Title: ER-beta: identification and characterization of a novel human estrogen receptor

A:Reference number: S71400; MUID:96354875; PMID:8769313

A:Accession: S71400

A:Molecule type: mRNA

A:Residues: 1-477 <MOS>

A:Cross-references: EMBL:X99101; NID:g1518262; PIDN:CAA67555.1; PID:g1518263

C:Superfamily: estrogen receptor; erba transforming protein homology

C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep

F:94-355/Domain: erba transforming protein homology <ERBA>

F:96-116/Region: zinc finger CCCC motif

F:132-156/Region: zinc finger CCCC motif

F:167-182/Region: nuclear location signal

F:52/Binding site: phosphate (Ser) (covalent) (by MAP kinase) #status predicted

F:96,99,113,116/Binding site: zinc (Cys) #status predicted

F:132,138,148,151/Binding site: zinc (Cys) #status predicted

Query Match 89.9%; Score 2522; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 7.5e-189;

Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 MNYISPSNVNLEGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPACEASL 113

Db 1 MNYISPSNVNLEGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPACEASL 60

Qy 114 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFF 173

Db 61 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFF 120

Qy 174 KRISIQGHNDYICPATNCTIDKNRKSQAACRLKCYEVMVKCGSRRCRGYLRVRQR 233

Db 121 KRISIQGHNDYICPATNCTIDKNRKSQAACRLKCYEVMVKCGSRRCRGYLRVRQR 180

Qy 234 SADEQLHCAGKAKRSQGHAPRVRELLDALSPEQLVTLLEAEPPHVLISRPSAPFTEAS 293

Db 181 SADEQLHCAGKAKRSQGHAPRVRELLDALSPEQLVTLLEAEPPHVLISRPSAPFTEAS 240

Qy 294 MMSLTAKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMGLMWSRIDHPGK 353

Db 241 MMSLTAKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMGLMWSRIDHPGK 300

Qy 354 LIFAPDLVLRDRGKCVGILFIDMLLATTSPRELAKHKEYLCVKAMILLNNSMYPL 413

Db 301 LIFAPDLVLRDRGKCVGILFIDMLLATTSPRELAKHKEYLCVKAMILLNNSMYPL 360

Qy 414 VTATQADSSRLKLAHLNNAVTDALVWVIAKSGISSQQSMRLANLLMLLSHVHRASNKG 473

Db 361 VTATQADSSRLKLAHLNNAVTDALVWVIAKSGISSQQSMRLANLLMLLSHVHRASNKG 420

Qy 474 EHLNKKCNVPPVYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSKGSONPQSQ 530

Db 421 EHLNKKCNVPPVYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSKGSONPQSQ 477

RESULT 3

JW0046

estrogen receptor beta2 - rat

N:Alternate names: ERbeta2

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 17-Mar-1999

C:Accession: JW0046

R:Maruyama, K.; Endoh, H.; Sasaki-Iwaka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.; Ki

Biochem. Biophys. Res. Commun. 246, 142-147, 1998

A:Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in

A:Reference number: JW0046; MUID:98262932; PMID:9600083

A:Accession: JW0046

A:Molecule type: mRNA

A:Residues: 1-503 <MAR>

A:Cross-references: DDBJ:AB012721

C:Comment: This protein functions as a negative regulator of estrogen action.

C:Superfamily: estrogen receptor; erba transforming protein homology

F:102-381/Domain: erba transforming protein homology <ERBA>

Query Match 81.4%; Score 2284; DB 2; Length 503;

Best Local Similarity 85.9%; Pred. No. 2.9e-170;

Matches 432; Conservative 23; Mismatches 30; Indels 18; Gaps 1;

Qy 46 MTFYSPAVWNYSTPSNVNLEGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 105

Db 1 MTFYSPAVWNYSTPSNVNLEGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 60

Qy 106 PWCEARSLHETLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSYASGYHYGVMS 165

Db 61 PWCEARSLHETLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSYASGYHYGVMS 120

Qy 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRKSQAACRLKCYEVMVKCGSRRCRG 225

Db 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRKSQAACRLKCYEVMVKCGSRRCRG 180

Qy 226 YRLVRQRSADEQLHCAGKAKRSQGHAPRVRELLDALSPEQLVTLLEAEPPHVLISR 285

Db 181 YRLVRQRSADEQLHCAGKAKRSQGHAPRVRELLDALSPEQLVTLLEAEPPHVLISR 240

Qy 286 SAPFTASMMMSITKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMGLM 345

Db 241 SAPFTASMMMSITKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMGLM 300

Qy 346 RSIDHPGKLIAPDLVLD-----RDGKCVGILFIDMLLATTSP 387

Db 301 RSIDHPGKLIAPDLVLDRSSDPHMHVAQMSAAPDEGKCVGILFIDMLLATTSP 360

Qy 388 RELKQHKVLCVKAMILLNNSMYPLVATQADSSRLKLAHLNNAVTDALVWVIAKSGIS 447

Db 361 RELKQHKVLCVKAMILLNNSMYPLASANQAESRKLTHLNNVTDALVWVIAKSGIS 420

Qy 448 SQQSQMRLANLLMLLSHVHRASNKGMEHLNKKCNVPPVYDILLLEMLNAHVLRGCKSSI 507

Db 421 SQQSQMRLANLLMLLSHVHRASNKGMEHLNKKCNVPPVYDILLLEMLNAHVLRGCKSSI 480

Qy 508 TGSECSPAEDSKSKGSONPQSQ 530

Db 481 SGSECSSTEDSKKNKSSQNLSQ 503

RESULT 4

ORCHE

estrogen receptor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 22-Jun-1999

C:Accession: A40914; S07182

R:Maxwell, B.D.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley,

Mol. Endocrinol. 1, 25-35, 1987

A:Title: Structural organization and regulation of the chicken estrogen receptor.

A:Reference number: A40914; MUID:88318621; PMID:2901032

A:Accession: A40914

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-589 <MAX>

R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.

EMBO J. 5, 891-897, 1986

A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human o

A:Reference number: S07192; MUID:86247578; PMID:3755102



```

RESULT 5
ORRHOE
estrogen receptor 1 - human
N;Alternate names: ER1; estrogen receptor alpha
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 23-Jun-1999
C;Accession: A94284; A93376; A43021; S27143; S34000; A41325; B41935; A03244; C41935; D41

```

F:185-205/Region: zinc finger CCCC motif  
F:221-245/Region: zinc finger CCCC motif  
F:300-595/Domain: steroid binding #status predicted <STB>  
F:236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.7%; Score 1224.5; DB 1; Length 595;  
Best Local Similarity 48.3%; Pred. No. 16-87;  
Matches 263; Conservative 88; Mismatches 129; Indels 55; Gaps 14;

QY 5 NSPSSLSNPSYNSQCSILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAMVNSIPS 60  
DB 21 NELEPLNRP-----QLKIPLERPLGEVYVDSS-----KPAVINYPEGAAY 74

QY 61 NVTNLEGGGRQ-----SIP-SNVTNLEGGGRQ-----TTSPNVLWPTQGHLSAP 101  
DB 75 Q-TGLPYGSGSAAAFSGNLGGFPPLNSVSPSLMLLHPPLQSPFLOPHGQVPPYLYE 133

QY 102 POKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPGP-----SKRDAHFCAVCS 154  
DB 134 NEPSGVTVREAGPPAFYRP--NSDNRQGGRRERLASTNDKSGMAMESAKETRYCAVCD 190

QY 155 YASGHYGVNSCEGCKAPFKRSIOGHNDYICPATNOCTIDKNRRKSCOACRLKCYEVM 214  
DB 191 YASGHYGVNSCEGCKAPFKRSIOGHNDYICPATNOCTIDKNRRKSCOACRLKCYEVM 250

QY 215 VKGSRERRCGVRLVRRQBSADEQLHCAGKAKRSQGHAPVR-----EL 258  
DB 251 MKGGIRKORRGGRMLKHKEQDD-----GEGRGEVSGAGDMRAANLWPSPLMKRSKNS 305

QY 259 LLDALSPQGLVTLLEAPPHVLSR--PSAPTEASMMSTKLADKELVHMISWAKKI 316  
DB 306 LALSUTADQWGSALLDAEPP--ILYSEYDTRFPLSEASMMGLLTNLADRELVHMISWAKRV 364

QY 317 PGFVELSLFDQVLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLVDRDEGKVEGILEI 376  
DB 365 PGFVDLTLDQVHLLSECAWLEILMIGLVMSMEHPVKLLFAPNLILDRNGKCVGMEVI 424

QY 377 FMKLATTSRFRRELKQHKYICVKAMILLNSMPLVTAT--QDASSRKLALHNAVTD 435  
DB 425 FMKLATTSRFRFMNLQGEFVCLKSIILNSGVYTFSLSTLKSLEEKDHIHRLVKTD 484

QY 436 ALVWVIAKSGISSQQSMELANLMLLSHVRIASNGMEHLNKKCNVVPVYDILLEKL 495  
DB 485 TIHLMAKAGLTLOQHQRLAQLLLILSHIRHWSKNGMEHLSMKCNVVPVYDILLEKL 544

QY 496 NAHVL 500  
DB 545 DAHRL 549

RESULT 6  
I47140  
estradiol receptor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text\_change 20-Aug-1999  
C:Accession: I47140; S66250; S32402  
R:Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.  
Mol. Cell. Endocrinol. 104, 163-172, 1994  
A:Title: The C-terminal half of the porcine estradiol receptor contains no post-translat  
A:Reference number: I47140; MUID:95080454; PMID:7988744  
A:Accession: I47140  
A:Status: preliminary; translated from GB/EXBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-595 <OK>  
A:Cross-references: EMBL:237167; NID:g587554; PIDN:CAA85524.1; PID:g587555  
A:Experimental source: uterus  
R:Thole, H.H.; Maschler, I.; Jungblut, P.W.  
Eur. J. Biochem. 231, 510-516, 1995  
A:Title: Surface mapping of the ligand-filled C-terminal half of the porcine estradiol r  
A:Reference number: S66250; MUID:95361877; PMID:7635163  
A:Accession: S66250  
A:Molecule type: protein  
A:Residues: 297-307;310-313;320-323;329-332;337-340;417-420;466-473 <THO>

A:Experimental source: uterus  
R:Thole, H.H.  
FEBS Lett. 320, 92-96, 1993  
A:Title: Assignment of the ligand binding site of the porcine estradiol receptor to th  
A:Reference number: S32402; MUID:93209384; PMID:8458437  
A:Accession: S32402  
A:Molecule type: Protein  
A:Residues: 303-323 <TH>  
A:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcript  
F:1-120/Domain: amino-terminal <NH2>  
F:121-299/Domain: DNA binding #status predicted <DNA>  
F:183-456/Domain: erba transforming protein homology <ERBA>  
F:185-205/Region: zinc finger CCCC motif  
F:221-245/Region: zinc finger CCCC motif  
F:256-271/Region: nuclear location signal  
F:300-595/Domain: steroid binding #status predicted <STB>  
F:185,188,202,205/Binding site: zinc (Cys) #status predicted  
F:221,227,237,240/Binding site: zinc (Cys) #status predicted  
F:236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.5%; Score 1219.5; DB 2; Length 595;  
Best Local Similarity 46.0%; Pred. No. 3-88-87;  
Matches 268; Conservative 89; Mismatches 126; Indels 99; Gaps 19;

QY 5 NSPSSLSNPSYNSQCSILPLEH--GSIYIPSSYVDSHHEYPAMTFYSPAMVNY----- 56  
DB 21 NELEPLNRP-----QLKIPLERPLGEVYVDSS-----KPAVINYPEGAAY 60

QY 57 -----SIP-SNVTNLEGGGRQ-----TTSPNVLWPTQGHLSAP 88  
DB 61 DFNAASAASAPVYQSGSLAYGPGSEAAAFANGLGQGPLNSVSPSLVLLHPPQLSPF 120

QY 89 LVVHRQLSHLYAEPKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPGP----- 141  
DB 121 LEPHGQGVPPYLENEPSGYAVREAGPPAFYRP--NSDNRQGGRRERLASTSDKSGMAE 177

QY 142 SKRDAHFCAVCSYASGHYGVNSCEGCKAPFKRSIOGHNDYICPATNOCTIDKNRRKSC 201  
DB 178 SAKTRYCAVNDYASGHYGVNSCEGCKAPFKRSIOGHNDYICPATNOCTIDKNRRKSC 237

QY 202 QACRLKCYEVMKVGKSGRRRCGRLVRRQBSADEQLHCAGKAK-----RSGG-- 250  
DB 238 QACRLKCYEVMKVGKSGRRRCGRLVRRQBSADEQLHCAGKAK-----GEGRNEAVPPGDMESANLW 292

QY 251 -----HAPVRELLLDALSPQGLVTLLEAPPHVLSR--PSAPTEASMMSTKL 301  
DB 293 PSPLLIKHKTCKNSPVL--SLTADQMISALLEAEPP--IYSEYDTRFPLSEASMMGLLTNL 349

QY 302 ADKELVHMISWAKKI PGFVELSLFDQVLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLV 361  
DB 350 ADRELVHMISWAKKI PGFVELSLFDQVLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLV 409

QY 362 LDRDEGKVEGILEI FMKLATTSRFRRELKQHKYICVKAMILLNSMPLVTAT--QDA 420  
DB 410 LDRNGKCVGMEVI FMKLATTSRFRFMNLQGEFVCLKSIILNSGVYTFSLSTLKS 469

QY 421 DSSRKLALHNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRIASNGMEHLNKKCNV 480  
DB 470 BEKHDIHRLVKTDITLHMAKAGLTLOQHQRLAQLLLILSHIRHWSKNGMEHLYNWK 529

QY 481 CNVVPVYDILLEKLNAHVLGCKSSITGSECSPAEDSKSKE 522  
DB 530 CNVVPVYDILLEKLNAHVLGCKSSITGSECSPAEDSKSKE 567

RESULT 7  
QRMSE  
estrogen receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 22-Jun-1999  
C:Accession: A40061  
R:White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.

Mol. Endocrinol. 1, 735-744, 1987  
A;Title: Structural organization and expression of the mouse estrogen receptor.  
A;Reference number: A40061; MID:91042558; PMID:2484714  
A;Accession: A40061  
A;Molecule type: mRNA  
A;Residues: 1-599 <WH1>  
A;Cross-references: GB:M38651; NID:G193179; PIDN:AAA37580.1; PID:G193180  
C;Comment: The steroid hormones and their receptors are involved in the regulation of e  
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit  
C;Superfamily: estrogen receptor; erba transforming protein homology  
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone rece  
F;1-183/Domain: amino-terminal <NH2>  
F;184-275/Domain: DNA binding #status predicted <DNA>  
F;187-210/Region: zinc finger CCCC motif  
F;223-245/Region: zinc finger CCCC motif  
F;260-275/Region: nuclear location signal  
F;304-556/Domain: steroid binding #status predicted <STB>  
F;189,192,206,209/Binding site: zinc (Cys) #status predicted  
F;225,231,241,244/Binding site: zinc (Cys) #status predicted  
F;240,309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.4%; Score 1218.5; DB 1; Length 599;  
Best Local Similarity 45.8%; Pred. No. 4.6e-87;  
Matches 263; Conservative 98; Mismatches 152; Indels 61; Gaps 14;

QY 5 NSPSSLSNSPSSYNCSQILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMYNYSIPS 60  
Db 21 NLELEPLNR-----QLKMPERALGEVYVDSKPTVNYPEGAAYEFNAFAAAAAAAGA 74

QY 61 NVTNLBG---GPGRQ-----TTSNVLWPTFGHLSPL-LVHRQLSHL 98  
Db 75 PVYQGSIAYGPGSEAAAFSANGSLGAPQLNSVSPSLMLLHPPLSPFLPHGQVFPY 134

QY 99 YASPOKSPWCEARSLHTLP---VNRRTLRKRVSGNRCAASPTVTPG-----SKRDAHFA 150  
Db 135 YLENEPS-----AVAVRTGPPAFYRSNDRRQNGRELSSNEKGNWIMESA 190

QY 151 VCSDYASGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQACRLRKCY 210  
Db 191 VCNDYASGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQACRLRKCY 250

QY 211 EVGMVKGSRRRCGVLEVRORSAD-----QLHCAGKAKRSG-----GHAPRVRE 257  
Db 251 EVGMVKGIRKRRGGMLKHKQRDDLEGRNEMGSGDMRAANLWPSPLVIGHTXKNSP 310

QY 258 LLLDALSPQLVLTLEAPPHVLIS-RPSAPTEASMMVSTKLADKELVHMISWAKKI 316  
Db 311 AL--SLTADQWVSALIDAEPPMIYSEYDPSRPTSEASMMGLLTNLADRELVLHMNAKRV 368

QY 317 PGFVELSLFDQVRLLESCEWVLMKLMWRSIDHPGKLIIFAPDLVLDSDGKCVGILEI 376  
Db 369 PGFDLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLIIFAPDLVLDSDGKCVGMEI 428

QY 377 FDMLLATTSRPRELKLQKVEYLCVKAMILLNSSMYPLVTAT-QDADSRLKLAHNAVTD 435  
Db 429 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDIHRVLDKTD 488

QY 436 ALVWIAKSGISGSOQSKNLANILMLLSHVHASNKGMEHLNNKCNVPTDILLEML 495  
Db 489 TLIHMAKAGLTLOOQHRLAQLLILSHIRHMSNKGMEHLNNKCNVPTDILLEML 548

QY 496 NAHVLRCXSSITGSCSPADSKSKSGSNQPS 529  
Db 549 DAHRLHAPARMGVPEPSTQATLTTSSSAHS 582

RESULT 8  
ORRTE  
estrogen receptor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1991 #sequence\_revision 14-Jul-1994 #text\_change 22-Jun-1999

C;Accession: S07379; S16731  
R;Koike, S.; Sakai, M.; Muramatsu, M.  
Nucleic Acids Res. 15, 2499-2513, 1987  
A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.  
A;Reference number: S07379; MID:87174780; PMID:3031601  
A;Accession: S07379  
A;Molecule type: mRNA  
A;Residues: 1-600 <KOI>  
A;Cross-references: EMBL:Y00102; NID:G56110; PIDN:CAA68287.1; PID:G56111  
R;Maggi, A.M.A.  
submitted to the EMBL Data Library, June 1991  
A;Reference number: S16731  
A;Accession: S16731  
A;Molecule type: mRNA  
A;Residues: 1-487, 'T', 489-600 <MAG>  
A;Cross-references: EMBL:X61098; NID:G56120; PIDN:CAA43411.1; PID:G56121  
C;Comment: The steroid hormones and their receptors are involved in the regulation of e  
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit  
C;Superfamily: estrogen receptor; erba transforming protein homology  
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone rece  
F;1-184/Domain: amino-terminal <NH2>  
F;185-276/Domain: DNA binding #status predicted <DNA>  
F;188-461/Domain: erba transforming protein homology <ERBA>  
F;188-211/Region: zinc finger CCCC motif  
F;224-246/Region: zinc finger CCCC motif  
F;261-276/Region: nuclear location signal  
F;305-557/Domain: steroid binding #status predicted <STB>  
F;190,193,207,210/Binding site: zinc (Cys) #status predicted  
F;226,232,242,245/Binding site: zinc (Cys) #status predicted  
F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.4%; Score 1216.5; DB 1; Length 600;  
Best Local Similarity 45.7%; Pred. No. 6.6e-87;  
Matches 262; Conservative 99; Mismatches 135; Indels 77; Gaps 17;

QY 5 NSPSSLSNSPSSYNCSQILPLEH--GSIYIPSYVDSHHEYPAMTFY-----SPAVMYN 56  
Db 21 NLELEPLNR-----QLKMPERALGEVYVDSN-KPAVFNYPGGAAYEFNAFAAAAAAAGA 73

QY 57 STP-----SNVTNLBGPGRQ-----TTSNVLWPTFGHLSPLV---V 91  
Db 74 SAPVYQGSSITY---GPGSEAAAFGANSGLGAPQLNSVSPSLMLLHPPHVSPFLPHG 130

QY 92 HQQLSHLYAEPQKSPWCEARSLHTLP---VNRRTLRKRVSGNRCAASPTVTPG-----SK 143  
Db 131 HQPYYLENEP-----SAYAVRTGPPAFYRSNDRRQNGRELSSSEKGNWIMESA 184

QY 144 RDAHPCAVCSYASGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQA 203  
Db 185 KETRYCAVCNDVASYGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQA 244

QY 204 CRLKCYEYGMVKGSRRRCGVLEVRORSAD-----QLHCAGKAKRSG-----G 250  
Db 245 CRLKCYEYGMVKGSRRRCGVLEVRORSAD-----QLHCAGKAKRSG-----G 304

QY 251 HAPRVRELLDALSPQLVLTLEAPPHVLIS-RPSAPTEASMMVSTKLADKELVHM 309  
Db 305 HTKKNSPAL--SLTADQWVSALIDAEPPMIYSEYDPSRPTSEASMMGLLTNLADRELVHM 362

QY 310 ISWAKKI PGFVELSLFDQVRLLESCEWVLMKLMWRSIDHPGKLIIFAPDLVLDSDGK 369  
Db 363 INWAKVPGFDLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLIIFAPDLVLDSDGK 422

QY 370 VEGILBIFDMLLATTSRPRELKLQKVEYLCVKAMILLNSSMYPLVTAT-QDADSRLKLAH 428  
Db 423 VEGVVEIFDMLLATTSRFRMNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDIHR 482

QY 429 LNAVTDALVWIAKSGISGSOQSKNLANILMLLSHVHASNKGMEHLNNKCNVPTV 488  
Db 483 VLDKINDTLIHLMAKAGLTLOOQHRLAQLLILSHIRHMSNKGMEHLNNKCNVPTV 542

QY 489 DILLEMLNAHVLRCXSSITGSCSPADSKSK 521

Db 543 DILLEMLDAHLHAPASRM--GVPEPESQSQ 572

RESULT 9

QXRLX

estrogen receptor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 28-Feb-1992 #sequence\_revision 14-Jul-1994 #text\_change 15-Jun-1996

C:Accession: A40907

R:Weiler, I.J.; Lew, D.; Shapiro, D.J.

Mol. Endocrinol. 1, 355-362, 1987

A:Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian re

A:Reference number: A40907; PMID:90331927; PMID:3274894

A:Accession: A40907

A:Molecule type: mRNA

A:Residues: 1-586 <WEI>

A:Cross-references: GB:L20735

C:Comment: In the steroid hormones and their receptors are involved in the regulation of eu

C:Complex appears to recognize discrete DNA sequences upstream of transcriptional start sit

C:Superfamily: estrogen receptor; erba transforming protein homology

C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep

F:1-174/Domain: amino-terminal <NH2>

F:175-266/Domain: DNA binding #status predicted <DNA>

F:178-448/Domain: erba transforming protein homology <ERBA>

F:178-201/Region: zinc finger CCCC motif

F:214-237/Region: zinc finger CCCC motif

F:251-266/Region: nuclear location signal

F:292-544/Domain: steroid binding #status predicted <STB>

F:180,183,197,200/Binding site: zinc (Cys) #status predicted

F:216,222,232,235/Binding site: zinc (Cys) #status predicted

F:233/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.3%; Score 1214; DB 1; Length 586;

Best Local Similarity 48.6%; Pred. No. 1e-86;

Matches 255; Conservative 82; Mismatches 138; Indels 50; Gaps 12;

Qy 36 YVDSH-----EYP-----AMTFYSPAMVNTSISNVTNEGGGRCQT-----TSP 76

Db 43 YVENRTGIFNYPEGTTVDFAAAAAPVYSSASLSAASSETFGSSLTGLHTLNVPSP 102

Qy 77 NVLWPTGHLSPVHVR-QLSHLYAEPQKSPCEARSLEHTLPVNRRLTKRKVSGNRCA 135

Db 103 VVFLAKLPQLSPFIHHGQVYLYESGQTFVAREAAPPTF-YRSSDNRQRSGRERMS 161

Qy 136 VWTGPG-----SKRDAHFCVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 190

Db 162 SANDKGPSPSMESTKTRYCAVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 221

Qy 191 CTIDNRRKSCQACRLKCYEVMKCGRRRCGYRLVRRORSADQLHCAGKAKRGSG 250

Db 222 CTIDNRRKSCQACRLKCYEVMKCGRRRCGYRLVRRORSADQLHCAGKAKRGSG 276

Qy 251 HA-----PRVRELLD---ALSPEQLVLTLEAPPHVLSRPSA-PFTTASMM 296

Db 277 PSEIRTAGIWNFVSKMGLSVLTAELISALMEAEPTVYSEHDSKPLSEASMMT 336

Qy 297 SITKLADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWSRIDHPGKLI 356

Db 337 LUTNLADRELVMINWAKKIPGFVDTLHDQVLLLECWLILWGLVLRVSRVHPGKLSF 396

Qy 357 APDLVLDREDEGKVEGILFIDMLLATTSPRFELKQHKYLCVKAMILLNSMYP 416

Db 397 APNLLDRNQRCEGLVEIFDMLVTTATRFPMFLRGEFEFICLSIILLNSGVYTFLLS 456

Qy 417 TQDADSSRLAH-LANAVTDALVWIAKSGISSQCSQSMRLANMLLMLSHVHRSNKGMEH 475

Db 457 TLESLEDTLIIHLLDKITDLVHWAKSGLSLQOQQLLQQLLILSHIRHMSNKGMEH 516

Qy 476 LLMKCNKQVVPVYDILLEMLNARHLRGCKSSITGSECSPAEDSKS 520

Db 517 LYSMKCNKQVVPVYDILLEMLNARHLRGCKSSITGSECSPAEDSKS 557

RESULT 10

T10423

estrogen receptor - Oryzias sp. (strain d-rr)

C:Species: Oryzias sp.

A:Variety: strain d-rr

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000

C:Accession: T10423

R:Okada, H.; Kawahara, T.; Yamashita, I.

submitted to the EMBL Data Library, March 1994

A:Description: Cloning of medaka estrogen receptor cDNA.

A:Reference number: Z17013

A:Accession: T10423

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-620 <OKA>

A:Cross-references: EMBL:D28954

A:Experimental source: strain d-rr, liver

C:Genetics:

A:Gene: MER

C:Superfamily: estrogen receptor; erba transforming protein homology

C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation

P:184-460/Domain: erba transforming protein homology <ERB>

Query Match 42.7%; Score 1199; DB 2; Length 620;

Best Local Similarity 48.1%; Pred. No. 1.e-85;

Matches 265; Conservative 81; Mismatches 129; Indels 76; Gaps 16;

Qy 36 YVDSHVEY-----PAMT-----FYSPAMVNTSIPS--NVTNLEGGGRCQTTPNVLW 80

Db 62 FLECTDYAAPNPATTPLYSOSTGYVSAPLETNGPPESEGLSGLSGSP----TSPLVFV 117

Qy 81 PTPGHLSPVHRLSHLYAEPQKSPCEARSLEHTLPVNRRLTKRKVSGNR----CASPV 137

Db 118 PSSPRLSPFM--HPPSHHLYETTTTPVYRSS-----HQASREDCQSSREDTCSLGE 167

Qy 138 TPGCS-----KRDAHFCVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 190

Db 168 LGAGAGAGGEMAKDTFCVACSDYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 227

Qy 191 CTIDNRRKSCQACRLKCYEVMKCGRRRCGYRLVRRQR-----SAD 236

Db 228 CTIDNRRKSCQACRLKCYEVMKCGRRRCGYRLVRRQR-----SAD 285

Qy 237 EQLHCAGKAKRS--GGHAPRVRELLDALSPEQLVLTLEAPPHVLSRSP--SAPTEA 292

Db 286 KTVHYDGRKSSSTGGGGGGGGRSLVTSIPPEQVLLLLQGAEP--ILCSRQLSRPTIEV 344

Qy 293 SMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWSRIDHPG 352

Db 345 TMTLTSTMAKELVHMSWAKKIPGFVLSLHDQVLLLESQWMEVLMGLMWSRIDHPG 404

Qy 353 KLIPAPDLVLDREDEGKVEGILFIDMLLATTSPRFELKQHKYLCVKAMILLNSMYP 412

Db 405 KLIPAPDLVLDREDEGKVEGILFIDMLLATTSPRFELKQHKYLCVKAMILLNSMYP 464

Qy 413 LVTATQD-ADSSRLAH-LANAVTDALVWIAKSGISSQCSQSMRLANMLLMLSHVHRSN 471

Db 465 FCTCTMEPLHNSAAVQSMLOTITDALHYISQSYLAQEAQARQAQLLLSHIRHMSN 524

Qy 472 GMEHLNKKCNKQVVPVYDILLEMLNARHLRGCKSSITGSECSPAE 516

Db 525 GMEHLNKKCNKQVVPVYDILLEMLNARHLRGCKSSITGSECSPAE 584

Qy 517 DSKSKEGSONP 527

Db 585 ISASRGRIESP 595

RESULT 11

S64737

80K estrogen receptor - human

C;Species: Homo sapiens (man)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Aug-1999  
C;Accession: S64737  
R;Pink, J.J.; Wu, S.Q.; Wolf, D.M.; Bilimoria, M.M.; Jordan, V.C.  
Nucleic Acids Res. 24, 962-969, 1996  
A;Title: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and 7  
A;Reference number: S64737; MUID:96174665; PMID:8600466  
A;Accession: S64737  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-701 <PIN>  
A;Cross-references: EMBL:U47678; NID:g1197854; PIDN:AAB00115.1; PID:g1197855  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996  
C;Superfamily: estrogen receptor; erba transforming protein homology  
C;Keywords: steroid hormone receptor; zinc finger  
F;183-456/Domain: erba transforming protein homology #status atypical <ERBA>  
F;518-562/Domain: erba transforming protein homology #status atypical <ERB2>

Query Match 41.9%; Score 1174.5; DB 2; Length 701;  
Best Local Similarity 41.2%; Pred. No. 1.5e-83;  
Matches 268; Conservative 87; Mismatches 125; Indels 171; Gaps 16;

Qy 5 NSPSSLNPSGYNCSQILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVNHYGPS 60  
Db 21 NELEPLNR-----OLKIPLERPLGEVYLDSSRPVAVNYPEGAAYEFNAAAANAQVYG 74  
Qy 61 NVTNLEGGPGRQ-----TTSNVLWPTPGHLSL-LVHRLSHLYAE 101  
Db 75 Q-TCLPTGPGSEAAAFSGNLGGFPPLNSVSPMLMLHPPQLSPFLOPHGQVPLYE 133  
Qy 102 PQKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPG-----SKRDAHFCAVCS 154  
Db 134 NEPSGYVREAGPAPFYRP--NSDNRQGRERLASTNDKGSMAESAKETRYCAVCSND 190  
Qy 155 YASGYHYGVMSCECKAPFKRSIOGHNDYICPATNCTIDKNRKSQACRLKCYEVGM 214  
Db 191 YASGYHYGVMSCECKAPFKRSIOGHNDYICPATNCTIDKNRKSQACRLKCYEVGM 250  
Qy 215 VKCSRRERCGRYLVRRQRSADEQLHCAGKAKRSQGHAPVR-----EL 258  
Db 251 MKGGRIRKRRGRMLKHKRQRD-----GEGRGVGSAGDMRAANLWPSPLMIKRSKNS 305  
Qy 259 LLDALSPQLVLTLEAEPPHLISR--PSAPTEASMMSLTKLADKELVHMSWAKKI 316  
Db 306 LAUSLTADQVSAALDAEPP--ILSYDYDTPRPFEASMGMLTLADRELVEHINNAKRV 364  
Qy 317 PGFVELSLFOVRLLESQWELMGLMWSIDHPGKLIIPAPDLVLDREGKCVGILEI 376  
Db 365 PGFVDTLHDQVHLLCAWLEILMGLVRSMEHPVKLLFAPNLLDRNQKCVGWEI 424  
Qy 377 FDMLLATSPRELKQHKYLCVKAMILLNSMYPLVAT-----QD----- 419  
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGYTFLSSTLRSLEEKDHIHRVLDKITD 484  
Qy 420 -----ADSSR----- 424  
Db 485 TLILHMAKAGLTQQQORLAQLLILSHIRHMRNQKCVGWEIFDMLLATSSRFMM 544  
Qy 425 -----KLAHLINAVTDALVWVIKSGISSQ 449  
Db 545 NLQGEFPVCLKSIILLNSGYTFLSSTLRSLEEKDHIHRVLDKITD TLILHMAKAGLTQ 604  
Qy 450 QQSRLANILLMLSHVHASNKGMEHLNKKCKQVVPYDILLEMNAHVL 500  
Db 605 QQHQRLAQLLILSHIRHMRNQKMEHLYSMKCKQVVPYDILLEMNAHVL 655

RESULT 12  
S58224  
oestrogen receptor - Atlantic salmon (fragment)  
C;Species: Salmo salar (Atlantic salmon)  
C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Aug-1999  
C;Accession: S58224

R;Rogers, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T.  
submitted to the EMBL Data Library, July 1995  
A;Reference number: S58224  
A;Accession: S58224  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-535 <ROG>  
A;Cross-references: EMBL:X89959; NID:g929901; PIDN:CAA61999.1; PID:g929902  
C;Superfamily: estrogen receptor; erba transforming protein homology  
C;Keywords: steroid hormone receptor; zinc finger  
F;103-382/Domain: erba transforming protein homology <ERBA>

Query Match 40.4%; Score 1134.5; DB 2; Length 535;  
Best Local Similarity 48.8%; Pred. No. 1.4e-80;  
Matches 246; Conservative 73; Mismatches 114; Indels 71; Gaps 15;

Qy 70 GROTTSNVLWPTPGHLSPLVHRLSH-----LYAEPKSPWCARSLEHTLPVNRRE 123  
Db 17 GSSPTGLVFSVSSPOLSPF-LHPPGHGLPSPSYLETSTPLYSVVVTLNLSAEE- 74  
Qy 124 LREKVGNCAS-PVTGPGSK-----RDAHFCAVCSGYHYGVMSCEGCKAFFKRSI 177  
Db 75 -KLCITSNRQQSVAAGSGVRVPEMANETRYCAVCSDFASGYHYGVMSCEGCKAFFKRSI 133  
Qy 178 QGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKGSRRCGRVLRVRRQSADE 237  
Db 134 QGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKGSLKDR--GGRVLRK-----D 187  
Qy 238 QLHC--AGKAKR-----SGGH-----APVRELLLDALSPQL 268  
Db 188 KRYCGPAGDREKPYGDEHTAPPQDGGRRNSSSSSUSGGGCGCPRI-----TMPPEQV 241  
Qy 269 VITLLBAEPPHVLISR--SAPTEASMMSLTKLADKELVHMSWAKKI PGFVELSLFD 326  
Db 242 LFLQGAEP-ALCSRKQVARPYETVMTLLTSMADKELVHMAWAKVPGFOELSLHD 300  
Qy 327 QVRLLESQWELMGLMWSIDHPGKLIIPAPDLVLDREGKCVGILEIFDMLLATTSR 386  
Db 301 QVQLLESQWELMGLMWSIDHPGKLIIPAPDLVLDREGKCVGILEIFDMLLATVSR 360  
Qy 387 FRELKLQHKYLCVKAMILLNSMYPLVT-ATODADSSRLKLAHLINAVTDALVWVIKSG 445  
Db 361 FRMLKLPBEFFVCLKSIILLNSGAPFCNSVESLHNSAVESMLNDITDALIHSHSG 420  
Qy 446 ISSQQSRLANILLMLSHVHASNKGMEHLNKKCKQVVPYDILLEMNAHVLRGCKS 505  
Db 421 ASVQQQPRQVQLLILSHIRHMRNQKMEHLYSMKCKQVVPYDILLEMNAHVLRGCKS 476  
Qy 506 SITGSECSAEDSKSKEGSONPOS 529  
Db 477 -----SPKVAQAGEQTEGPF 493

RESULT 13  
A37197  
estrogen receptor - rainbow trout  
C;Species: Oncorhynchus mykiss (rainbow trout)  
C;Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 20-Aug-1999  
C;Accession: A37197; A40070  
R;Pakdel, F.; Le Gac, F.; Le Goff, P.; Valotaire, Y.  
Mol. Cell. Endocrinol. 71, 195-204, 1990  
A;Title: Full-length sequence and in vitro expression of rainbow trout estrogen receptor  
A;Reference number: A37197; MUID:91006824; PMID:2210031  
A;Accession: A37197  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-574 <PAK>  
A;Cross-references: GB:M31559  
R;Pakdel, F.; Le Guellec, C.; Vaillant, C.; Le Roux, M.G.; Valotaire, Y.  
Mol. Endocrinol. 3, 44-51, 1989  
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger  
A;Reference number: A40070; MUID:89127284; PMID:2515848  
A;Accession: A40070



Qy 441 IAKSGISSQQQSRLANLMLLSHVHRHASNKGMEHLINMKCKNVVPVYDILLLEMLNAHV 499  
Db 380 -----SORHEPRRAGKLIWTLPLLRQTAATAKAVQHPFYSVKLGKVPVPHKLFLEMLEAKV 433

Search completed: June 20, 2004, 10:39:11  
Job time : 22 secs

GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: June 20, 2004, 10:31:17 ; Search time 17 Seconds  
(Without alignments)  
1623.364 Million cell updates/sec

Title: US-08-906-365-2  
Perfect score: 2805  
Sequence: 1 MDIKSPSLNPSPPSYNCQ.....ECSPAEDSKSKEGSONPOSQ 530

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	100.0	530	1 ESR2 HUMAN	Q92731 homo sapien
2	2615	93.2	530	1 ESR2 CALJA	Q95171 callithrix
3	2496	89.0	530	1 ESR2 RAT	Q62986 rattus norv
4	2495	88.9	530	1 ESR2 MOUSE	Q08537 mus musculus
5	2463.5	87.5	527	1 ESR2 BOVIN	Q9xsb5 bos taurus
6	2455.5	87.8	527	1 ESR2 SHEEP	Q9tuls ovis aries
7	2415	86.1	526	1 ESR2 PIG	Q9xsw2 sturnus vul
8	2101	74.9	554	1 ESR2 STUVU	Q9pve2 sturnus vul
9	1959	69.8	472	1 ESR2 COTJA	Q93511 coturnix co
10	1948.5	69.5	472	1 ESR2 CHICK	Q9ptu5 gallus gall
11	1549	55.2	573	1 ESR2 ANGJA	Q13012 anguilla ja
12	1466	52.3	568	1 ESR1 CARAU	Q9w869 carassius a
13	1440.5	51.4	568	1 ESR2 ONCMY	P57782 oncorhynch
14	1431	51.0	673	1 ESR2 MICUN	P57781 micropogoni
15	1398	49.8	279	1 ESR2 MACMU	Q9ttem macaca mul
16	1385.5	49.4	559	1 ESR2 SPAAU	Q9w6m2 sparus aua
17	1381	49.2	575	1 ESR2 ICTPU	Q9iak1 ictalurus p
18	1378.5	49.1	610	1 ESR2 CARAU	Q9ial9 carassius a
19	1373	48.9	585	1 ESR2 MICUN	P57783 micropogoni
20	1352	48.2	557	1 ESR2 ORENI	Q9yh32 oreochromis
21	1233.5	44.0	595	1 ESR1 HUMAN	P03372 homo sapien
22	1228.5	43.8	597	1 ESR1 POEGU	Q91250 poephilia gu
23	1225.5	43.7	589	1 ESR1 CHICK	P06212 gallus gall
24	1220	43.5	594	1 ESR1 HORSE	Q9tv98 equus caball
25	1219.5	43.5	595	1 ESR1 PIG	Q29040 sus scrofa
26	1219	43.5	595	1 ESR1 MESAU	Q9qzj5 mesocricetu
27	1218.5	43.4	599	1 ESR1 MOUSE	P19785 mus musculus
28	1216.5	43.4	600	1 ESR1 RAT	P06211 rattus norv
29	1214	43.3	585	1 ESR1 ORENI	Q9yh33 oreochromis
30	1214	43.3	586	1 ESR1 XENLA	P81559 xenopus lae
31	1210	43.1	569	1 ESR1 BRARE	P57717 brachydanio
32	1204	42.9	579	1 ESR1 SPAAU	Q9pv29 sparus aua
33	1199	42.7	620	1 ESR1 ORYLA	P50241 oryzias lat

#### ALIGNMENTS

##### RESULT 1

ID	ESR2 HUMAN	STANDARD;	PRT:	530 AA.
AC	Q92731; Q60608; Q60685; Q60702; Q60703; Q75583; Q75584; Q9UEV6;			
AC	Q9UHD3; Q9UQK9;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Estrogen receptor beta (ER-beta).			
GN	ESR2 OR NR3A2 OR ESR2B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=98139878; PubMed=9473491;			
RA	Ogawa S., Inoue S., Watanabe T., Hiroi H., Orimo A., Hosoi T.,			
RA	Ouchi Y., Muramatsu M.;			
RT	"The complete primary structure of human estrogen receptor beta			
RT	(hERbeta) and its heterodimerization with ER alpha in vivo and in			
RT	vitro.";			
RL	Biochem. Biophys. Res. Commun. 243:122-126(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RC	TISSUE=Breast, and Testis;			
RX	MEDLINE=98300286; PubMed=9636657;			
RA	Moore J.T., McKee D.D., Slentz-Kesler K., Moore L.B., Jones S.A.,			
RA	Horne B.L., Su J.-L., Klierer S.A., Lehmann J.M., Willson T.M.;			
RT	"Cloning and characterization of human estrogen receptor beta			
RT	isoforms.";			
RL	Biochem. Biophys. Res. Commun. 247:75-78(1998).			
RN	[3]			
RP	SEQUENCE OF 48-530 FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.			
RC	TISSUE=Testis;			
RX	MEDLINE=98354875; PubMed=8769313;			
RA	Mosselman S., Polman J., Dijkema R.;			
RT	"ER beta: identification and characterization of a novel human			
RT	estrogen receptor.";			
RL	FEBS Lett. 392:49-53(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.			
RC	TISSUE=Testis;			
RX	MEDLINE=98337908; PubMed=9671811;			
RA	Ogawa S., Inoue S., Watanabe T., Orimo A., Hosoi T., Ouchi Y.,			
RA	Muramatsu M.;			
RT	"Molecular cloning and characterization of human estrogen receptor			
RT	beta cx: a potential inhibitor of estrogen action in human.";			
RL	Nucleic Acids Res. 26:3505-3512(1998).			
RN	[5]			
RP	SEQUENCE OF 59-530 FROM N.A. (ISOFORMS 7 AND 8).			
RC	TISSUE=Endometrium;			
RX	Brandenberger A.W., Lebovic D., Taylor R.N., Jaffe R.B.;			
RL	Submitted [JUN-1998] to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			

34	1194.5	42.6	581	1	ESR1 PAGMA	O42132 pagrus majo
35	1184.5	42.2	583	1	ESR1 OREAU	P50240 oreochromis
36	1177	42.0	525	1	ESR1 MICUN	P57753 micropogoni
37	1165	41.5	622	1	ESR1 ONCMY	P16058 oncorhynch
38	1160.5	41.4	617	1	ESR1 ICTPU	Q9yhz7 ictalurus p
39	1134.5	40.4	535	1	ESR1 SALSA	P50242 salmo salar
40	877	31.3	307	1	ESR1 CNEUN	Q91424 cnemidophor
41	799.5	28.5	349	1	ESR1 ANOCA	Q9yht3 anolis caro
42	648	23.1	458	1	ESR3 HUMAN	O75454 homo sapien
43	631.5	22.5	433	1	ERR2 RAT	P11475 rattus norv
44	630	22.5	500	1	ERR2 HUMAN	O95718 homo sapien
45	619.5	22.1	433	1	ERR2 MOUSE	Q61539 mus musculus



CC TISSUE-Ovary;  
 CC MEDLINE=98348389; PubMed=9685228;  
 CC Lu B., Leygue E., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H.;  
 CC "Estrogen receptor-beta mRNA variants in human and murine tissues";  
 CC Mol. Cell. Endocrinol. 138:199-203(1998).  
 CC [7]  
 CC SEQUENCE OF 1-69 FROM N.A.  
 CC Li L.C., Dahiya R.;  
 CC "Cloning and characterization of the estrogen receptor beta gene  
 CC promoter.";  
 CC J. Biol. Chem. 272:25832-25838(1997).  
 CC [8]  
 CC CHARACTERIZATION.  
 CC MEDLINE=97467383; PubMed=9325313;  
 CC Pace P., Taylor J., Suntharalingam S., Coombes R.C., Ali S.;  
 CC "Human estrogen receptor beta binds DNA in a manner similar to and  
 CC dimerizes with estrogen receptor alpha.";  
 CC J. Biol. Chem. 272:25832-25838(1997).  
 CC [9]  
 CC INTERACTION WITH NCOA3.  
 CC MEDLINE=97410321; PubMed=9267036;  
 CC Chen H., Lin R.J., Schiltz R.L., Chakravarti D., Nash A., Nagy L.,  
 CC Privalsky M.L., Nakatani Y., Evans R.M.;  
 CC "Nuclear receptor coactivator ACTR is a novel histone  
 CC acetyltransferase and forms a multimeric activation complex with P/CAP  
 CC and CBP/p300.";  
 CC Cell 90:569-580(1997).  
 CC [10]  
 CC INTERACTION WITH NCOA6.  
 CC MEDLINE=20148724; PubMed=10681503;  
 CC Calra F., Antonson P., Pellico-Huikko M., Treuter E., Gustafsson J.-A.;  
 CC "Cloning and characterization of RAP250, a nuclear receptor  
 CC coactivator.";  
 CC J. Biol. Chem. 275:5308-5317(2000).  
 CC [11]  
 CC INTERACTION WITH NCOA5.  
 CC MEDLINE=20565767; PubMed=11113208;  
 CC Sauve F., McBroome L.D.B., Gallant J., Moraitis A.N., Labrie F.,  
 CC Giguere V.;  
 CC "CRA, a novel estrogen receptor coactivator with a bifunctional  
 CC nuclear receptor interacting determinant.";  
 CC Mol. Cell. Biol. 21:343-353(2001).  
 CC -!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an  
 CC affinity similar to that of ESR1, and activates expression of  
 CC reporter genes containing estrogen response elements (ERE) in an  
 CC estrogen-dependent manner. Isoform beta-2 lacks ligand binding  
 CC ability and has no or only very low binding activity resulting  
 CC in the loss of ligand-dependent transactivation ability. DNA-  
 CC binding by ESR1 and ESR2 is rapidly lost at 37 degrees Celsius in  
 CC the absence of ligand while in the presence of 17 beta-estradiol  
 CC and 4-hydroxy-tamoxifen loss in DNA-binding at elevated  
 CC temperature is more gradual.  
 CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
 CC ESR1. Isoform beta-2/cx preferentially forms a heterodimer with  
 CC ESR1 rather than ESR2 and inhibits DNA-binding by ESR1. Interacts  
 CC with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong  
 CC increase of transcription of target genes.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=8;  
 CC Name=1; Synonyms=Beta-1;  
 CC IsoId=Q92731-1; Sequences=Displayed;  
 CC Name=2; Synonyms=Beta-2, CX;  
 CC IsoId=Q92731-2; Sequences=VSP\_003689;  
 CC Name=3; Synonyms=Beta-2A;  
 CC IsoId=Q92731-3; Sequences=VSP\_003684, VSP\_003686;  
 CC Name=4; Synonyms=Beta-3;  
 CC IsoId=Q92731-4; Sequences=VSP\_003690;  
 CC Name=5; Synonyms=Beta-4;  
 CC IsoId=Q92731-5; Sequences=VSP\_003691;  
 CC Name=6; Synonyms=Beta-5;  
 CC IsoId=Q92731-6; Sequences=VSP\_003692;  
 CC Name=7; Synonyms=Beta-5A;  
 CC IsoId=Q92731-7; Sequences=VSP\_003685;  
 CC Name=8; Synonyms=Beta-6;  
 CC IsoId=Q92731-8; Sequences=VSP\_003697, VSP\_003698;  
 CC TISSUE SPECIFICITY: Isoform beta-1 is expressed in testis and  
 CC ovary, and at a lower level in heart, brain, placenta, liver,  
 CC skeletal muscle, spleen, thymus, prostate, colon, bone marrow,  
 CC mammary gland and uterus. Also found in uterine bone, breast, and  
 CC ovarian tumor cell lines, but not in colon and liver tumors.  
 CC Isoform beta-2 is expressed in spleen, thymus, testis and ovary  
 CC and at a lower level in skeletal muscle, prostate, colon, small  
 CC intestine, leukocytes, bone marrow, mammary gland and uterus.  
 CC Isoform beta-3 is found in testis. Isoform beta-4 is expressed in  
 CC testis, and at a lower level in spleen, thymus, ovary, mammary  
 CC gland and uterus. Isoform beta-5 is expressed in testis, placenta,  
 CC skeletal muscle, spleen and leukocytes, and at a lower level in  
 CC heart, lung, liver, kidney, pancreas, thymus, prostate, colon,  
 CC small intestine, bone marrow, mammary gland and uterus. Not  
 CC expressed in brain.  
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
 CC a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AB006590; BAA24953.1; -  
 CC EMBL; AF051427; AAC05985.1; -  
 CC EMBL; AF051428; AAC05951.1; -  
 CC EMBL; AF061054; AAC39784.1; -  
 CC EMBL; AF061055; AAC39785.1; -  
 CC EMBL; AF060555; AAC15234.1; -  
 CC EMBL; X99101; CAA67555.1; ALT\_INIT.  
 CC EMBL; AB006589; BAA31966.1; -  
 CC EMBL; AF074598; AAC25602.1; -  
 CC EMBL; AF074599; AAC25603.1; -  
 CC EMBL; AF124790; AAC32580.1; -  
 CC EMBL; AF07463; AAC03786.1; -  
 CC EMBL; AF191544; AAF24232.1; -  
 CC PDB; 1L2J; 01-MAY-02.  
 CC PDB; 1NDE; 18-DEC-02.  
 CC PDB; 1QKW; 28-JUL-00.  
 CC TRANSFAC; T04651; -  
 CC TRANSFAC; T05387; -  
 CC TRANSFAC; T05388; -  
 CC TRANSFAC; T05389; -  
 CC TRANSFAC; T05390; -  
 CC TRANSFAC; T05391; -  
 CC Gene; HGNC:3469; ESR2.  
 CC MIM; 601663; -  
 CC GO; GO:0005634; C:nucleus; TAS.  
 CC GO; GO:0030284; P:estrogen receptor activity; TAS.  
 CC GO; GO:0048019; P:receptor antagonist activity; NAS.  
 CC GO; GO:0005496; P:steroid binding; TAS.  
 CC GO; GO:0003700; P:transcription co-activator activity; TAS.  
 CC GO; GO:0003700; P:transcription factor activity; TAS.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0030520; P:estrogen receptor signaling pathway; TAS.  
 CC GO; GO:0030308; P:negative regulation of cell growth; NAS.  
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.  
 CC GO; GO:0007155; P:signal transduction; TAS.  
 CC InterPro; IPR000536; Hormone\_rec\_lig.  
 CC InterPro; IPR001723; Steroid\_receptor.  
 CC InterPro; IPR008946; Str\_ncl\_receptor.  
 CC InterPro; IPR001628; Znf\_C4steroid.  
 CC Pfam; PF00104; hormone\_rec; 1.  
 CC Pfam; PF00105; zf-C4; 1.  
 CC PRINTS; PR00398; STERHORMONER.

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Query Match      100.0%; Score 2805; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYNYSIPS 60
Db 1 MDIKNSPSSLNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYNYSIPS 60
Qy 61 NVTNLEGGPGRTTSNVLWPTGHLSPVYVHQLSHLYAEPKSPWCEARSLEHTLPVN 120
Db 61 NVTNLEGGPGRTTSNVLWPTGHLSPVYVHQLSHLYAEPKSPWCEARSLEHTLPVN 120
Qy 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGYHYGWSCEGCKAFKRSIQGH 180
Db 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGYHYGWSCEGCKAFKRSIQGH 180
Qy 181 NDYICPATNQCTTDKRRKSCQACRLKCYEVGMVKGSRRCGYLVRQRSADEQLH 240
Db 181 NDYICPATNQCTTDKRRKSCQACRLKCYEVGMVKGSRRCGYLVRQRSADEQLH 240
Qy 241 CAGKAKSGGHAPRVRELLDALSPEQLVTLLEAEPHVLISRPAPFTFASMMSLTK 300
Db 241 CAGKAKSGGHAPRVRELLDALSPEQLVTLLEAEPHVLISRPAPFTFASMMSLTK 300
Qy 301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCHWMEVLMGLMWRSIDHPGKLIAPDL 360
Db 301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCHWMEVLMGLMWRSIDHPGKLIAPDL 360
Qy 361 VLORDEGKCVGEGILEIFDMLLATTSRFRLEKQHEVLCVKAMILLNSSMYPLVTATQDA 420
Db 361 VLORDEGKCVGEGILEIFDMLLATTSRFRLEKQHEVLCVKAMILLNSSMYPLVTATQDA 420
Qy 421 DSSRKLHLNAVTDALVWVIAKSGISSQQSQSMELANLEMLLGHVHSHASNGHEHLINMK 480
Db 421 DSSRKLHLNAVTDALVWVIAKSGISSQQSQSMELANLEMLLGHVHSHASNGHEHLINMK 480
Qy 481 CKNVVPYDILLEMVNAHVLRGCKSSITGSECSPAEDSKSGESQNPQSQ 530
Db 481 CKNVVPYDILLEMVNAHVLRGCKSSITGSECSPAEDSKSGESQNPQSQ 530

RESULT 2
ESR2_CALJA STANDARD; PRT; 530 AA.
ID ESR2_CALJA
AC Q95171;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.
CX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Testis;
RA Gaughan J., Scobie G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
affinity similar to that of ESR1 (ER-alpha), and activates
expression of reporter genes containing estrogen response elements
(SRE) in an estrogen-dependent manner. May play a role in ovarian
follicular growth and maturation.
-!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
ESR1. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
to a strong increase of transcription of target genes (By
similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.

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-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
subfamily.
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or send an email to license@isb-sib.ch).
EMBL; Y09372; CAA70546.2; -
HSP; P03372; LHQ.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:0030284; F:estrogen receptor activity; ISS.
GO; GO:0048079; F:ligand-dependent nuclear receptor activity; ISS.
GO; GO:0048019; F:receptor antagonist activity; ISS.
GO; GO:0005496; F:steroid binding; ISS.
GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
GO; GO:0030308; P:negative regulation of cell growth; ISS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Steroid_receptor.
InterPro; IPR008946; Str_ncl_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STERDORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOL1_1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding; Phosphorylation.
FT DOMAIN 1 148 NUCLEAR RECEPTOR-TYPE.
FT ZN BIND 149 214 C4-TYPE.
FT ZN BIND 149 169 C4-TYPE.
FT ZN BIND 185 209 C4-TYPE.
FT ZN BIND 215 530 STEROID-BINDING.
FT MOD RES 87 87 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 488 488 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 530 AA; 59087 MW; 45D89107A84C53D1 CRC64;

Query Match      93.2%; Score 2615; DB 1; Length 530;
Best Local Similarity 92.4%; Pred. No. 6.2e-200;
Matches 489; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYNYSIPS 60
Db 1 MDIKNSPSSLNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYNYSIPS 60
Qy 61 NVTNLEGGPGRTTSNVLWPTGHLSPVYVHQLSHLYAEPKSPWCEARSLEHTLPVN 120
Db 61 NVTNLEGGPGRTTSNVLWPTGHLSPVYVHQLSHLYAEPKSPWCEARSLEHTLPVN 120
Qy 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGYHYGWSCEGCKAFKRSIQGH 180
Db 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGYHYGWSCEGCKAFKRSIQGH 180
Qy 181 NDYICPATNQCTTDKRRKSCQACRLKCYEVGMVKGSRRCGYLVRQRSADEQLH 240
Db 181 NDYICPATNQCTTDKRRKSCQACRLKCYEVGMVKGSRRCGYLVRQRSADEQLH 240
Qy 241 CAGKAKSGGHAPRVRELLDALSPEQLVTLLEAEPHVLISRPAPFTFASMMSLTK 300
Db 241 CAGKAKSGGHAPRVRELLDALSPEQLVTLLEAEPHVLISRPAPFTFASMMSLTK 300
Qy 301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCHWMEVLMGLMWRSIDHPGKLIAPDL 360
Db 301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCHWMEVLMGLMWRSIDHPGKLIAPDL 360
Qy 361 VLORDEGKCVGEGILEIFDMLLATTSRFRLEKQHEVLCVKAMILLNSSMYPLVTATQDA 420

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DB 361 ILDRDEGKCVGILFVFMLLATTSFRFELKQHEYLVCVAMVLLNSQYDPLVATQDA 420  
QY 421 DSSKRLAHLNAVTDALVWVITAKSGISQOQSMRLANLLMLLSHVHRASNKGMHLLNMK 480  
DB 421 ESSQKLAHLNAVTDALVWVITAKSGFSQOQSVRLANLLMLLSHVHRASNKGMHLLSMK 480  
QY 481 CKNVVVYDLEMLNAHVLGCKSGISITGSCSPAEDSKSKEGSONPOS 529  
DB 481 CKNVVVYDLEMLNAHVLGCKSGISITGSCSPAEDSKSKEGSONPOS 529  
RESULT 3  
ESR2\_RAT  
ID ESR2\_RAT STANDARD; PRT: 530 AA.  
Q62986; O35784; O35785; O55015; O55016; O70195; Q9R185;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Estrogen receptor beta (ER-beta).  
GN ESR2 OR NR3A2 OR ERBETA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE OF 46-530 FROM N.A. (ISOFORM 1).  
RC STRAIN=Sprague-Dawley; TISSUE=Prostate;  
RX MEDLINE=96234066; PubMed=8650195;  
RA Kuper G.G.J.M., Enmark E., Peltto-Huikko M., Nilsson S.,  
RA Gustafsson J.-A.;  
RT "Cloning of a novel receptor expressed in rat prostate and ovary."  
RL Proc. Natl. Acad. Sci. U.S.A. 93:5925-5930(1996).  
RN [2]  
RP SEQUENCE OF 46-530 FROM N.A. (ISOFORM 2).  
RC STRAIN=Wistar; TISSUE=Ovary;  
RX MEDLINE=96262932; PubMed=9600083;  
RA Maruyama K., Endoh H., Sasaki-Iwacka H., Kanou H., Shimaya E.,  
RA Hashimoto S., Kato S., Kawashima H.;  
RT "A novel isoform of rat estrogen receptor beta with 18 amino acid  
RT insertion in the ligand binding domain as a putative dominant  
RT negative regulator of estrogen action".  
RL Biochem. Biophys. Res. Commun. 246:142-147(1998).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=Wistar; TISSUE=Prostate;  
RA Aldridge T.C.;  
RT "Tissue specific responses to estrogen: an explanation based on  
RT differential activation of multiple estrogen receptors with different  
RT estrogen response elements".  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 46-530 FROM N.A. (ISOFORMS 1; 3 AND 4).  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=98151005; PubMed=9492041;  
RA Petersen D.N., Thalcevic G.T., Kozar-Taylor P.H., Turi T.G.,  
RA Brown T.A.;  
RT "Identification of estrogen receptor beta2, a functional variant of  
RT estrogen receptor beta expressed in normal rat tissues".  
RL Endocrinology 139:1082-1092(1998).  
RN [5]  
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 5).  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RA Price R., Handa R.J.;  
RT "A novel splice variant of estrogen receptor beta found in rat  
RT brain".  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Binds estrogens with an affinity similar to that of ER-  
CC ALPHA, and activates expression of reporter genes containing  
CC estrogen response elements (ERE) in an estrogen-dependent manner.  
CC Isoform 3 and isoform 4 are unable to bind DNA and activate  
CC transcription due to the truncation of the DNA binding domain.  
CC Isoform 2 shows loss of ligand binding affinity and suppresses ER-

ALPHA and ER-BETA mediated transcriptional activation and may act  
as a dominant negative regulator of estrogen action.  
-!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
ESR1. Can also form heterodimers with isoforms 1 and 2.  
CC Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a  
CC strong increase of transcription of target genes (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=5;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1; Synonyms=Beta1;  
CC IsoId=Q62986-1; Sequence=Displayed;  
CC Name=2; Synonyms=Beta2;  
CC IsoId=Q62986-2; Sequence=VSP\_003699;  
CC Name=3; Synonyms=Beta1-delta3; Sequence=VSP\_003697;  
CC IsoId=Q62986-3; Sequence=VSP\_003697;  
CC Name=4; Synonyms=Beta2-delta3;  
CC IsoId=Q62986-4; Sequence=VSP\_003697; VSP\_003699;  
CC Name=5; Synonyms=Beta1-delta4;  
CC IsoId=Q62986-5; Sequence=VSP\_003698;  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, OVARY, LUNG, LIVER,  
CC KIDNEY, FAT, BONE, BRAIN, UTERUS AND TESTIS.  
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
CC a DNA-binding domain and a C-terminal steroid-binding domain.  
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
CC subfamily.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EXBL: U57439; AAC52602.1; -  
CC EXBL: AB012721; BAA25431.1; -  
CC EXBL: AJ002602; CAA05631.1; ALT\_INIT.  
CC EXBL: AJ002603; CAA05632.1; -  
CC EXBL: AF042058; AAB97424.1; -  
CC EXBL: AF042059; AAB97425.1; -  
CC EXBL: AF042060; AAB97426.1; -  
CC EXBL: AF042061; AAB97427.1; -  
CC EXBL: AF161187; AAD47637.1; -  
CC EDE; IHJ1; 04-JAN-02.  
CC PDB; 1QKN; 28-JUL-00.  
CC GO; GO:0005634; C:nucleus; ISS.  
CC GO; GO:0030284; F:estrogen receptor activity; ISS.  
CC GO; GO:0004879; F:ligand-dependent nuclear receptor activity; ISS.  
CC GO; GO:0048019; F:receptor antagonist activity; ISS.  
CC GO; GO:0035496; P:steroid binding; ISS.  
CC GO; GO:0030520; P:steroid receptor signaling pathway; ISS.  
CC GO; GO:0030308; P:negative regulation of cell growth; ISS.  
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
CC InterPro; IPR000536; Hormone\_rec\_lig.  
CC InterPro; IPR001723; Sterhmrn\_receptor.  
CC InterPro; IPR008946; Str\_ncl\_receptor.  
CC InterPro; IPR01628; Znf\_C4steroid.  
CC Pfam; PF00104; hormone\_rec; 1.  
CC Pfam; PF00105; zf-C4; 1.  
CC PRINTS; PR00398; STRDHORMONER.  
CC PRINTS; PR00047; STROIDFINGER.  
CC ProDom; PD000035; Znf\_C4steroid; 1.  
CC SMART; SM00430; HOL1; 1.  
CC SMART; SM00399; Znf\_C4; 1.  
CC PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
CC Zinc-finger; Steroid-binding; Alternative splicing; Phosphorylation;  
CC 3D-structure.  
FT DOMAIN 1 148 MODULATING.  
FT DNA\_BIND 149 214 NUCLEAR RECEPTOR-TYPE.  
FT ZN\_FING 149 169 C4-TYPE.  
FT ZN\_FING 185 209 C4-TYPE.  
FT

FT	DOMAIN	215	530	STERIOD-BINDING.
FT	MOD_RES	87		PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	488		PHOSPHORYLATION (BY SIMILARITY).
FT	VARSPLIC	179	217	Missing (in isoform 3 and isoform 4).
FT				/FtId=VSP 003697.
FT	VARSPLIC	219	318	Missing (in isoform 5).
FT				/FtId=VSP 003698.
FT	VARSPLIC	364	364	R -> RSSEDPHHVAQMSAADR (in isoform 2 and isoform 4).
FT				/FtId=VSP 003699.
FT	CONFLICT	72		L -> Q (IN REF. 3 AND 4).
FT	CONFLICT	150		P -> A (IN REF. 3 AND 4).
FT	CONFLICT	165		S -> P (IN REF. 3; CAA05631).
FT	CONFLICT	505		S -> P (IN REF. 3; CAA05631).
SQ	SEQUENCE	530 AA;	59152 MW;	36F269D9FD773DA9 CRC64;
Query Match				
Best local similarity		89.08;	Score 2496;	DB 1; Length 530;
Matches 468; Conservative		88.34;	Pred. No. 1.7e-190;	
			Mismatches 35;	Indels 0; Gaps 0;
Qy	1	MDIKNSPSSLSNPSYNCOSILPLEHSGIYIPSSYVDSHHEYPAMTFYSPAVMYNTSIPS	60	
Db	1	MEIKNSPSSLSNPSYNCOSILPLEHSGIYIPSSYVDSHHEYPAMTFYSPAVMYNTSIPS	60	
Qy	61	NTNLEGGPQRTSPNVLPWPTPGHLSPLVHQLSHLYABPOKSPWCCEARSLEHTLPVN	120	
Db	61	STGNLDGPPVRLTSPNVLPWPTPGHLSPLVHQLSHLYABPOKSPWCCEARSLEHTLPVN	120	
Qy	121	RETLKRVKSGNRCASPTVPGSKRDHAFCAVSDYASGYHYGVNSCEGCKAFKRSIQGH	180	
Db	121	RETLKRLKSSGSCASPTVSNAKDAEFCVSDYASGYHYGVNSCEGCKAFKRSIQGH	180	
Qy	181	NDVICPATNCTIDKNRKSCQACRLKCYEVGMVKCGSRRCRGYELVRRQSRADQLH	240	
Db	181	NDVICPATNCTIDKNRKSCQACRLKCYEVGMVKCGSRRCRGYELVRRQSRADQLH	240	
Qy	241	CAGKAKSGGHAPVRELLDALSPEQLVLTLEAEPPHVLISRPSPAPPTFASMMSLTK	300	
Db	241	CLSKAKNGGHAPVRELLDALSPEQLVLTLEAEPPHVLISRPSPAPPTFASMMSLTK	300	
Qy	301	LADKELVHMSIWAKKIPGFVLSLFDQVRLLESCEWMEVLMMGLMWSRIDHPGKLIAPDL	360	
Db	301	LADKELVHMGWAKKIPGFVLSLFDQVRLLESCEWMEVLMMGLMWSRIDHPGKLIAPDL	360	
Qy	361	VLDRECKVEGILEIFDMLLATTSPRELKLOHKEVLCUKAMILLNSSMYPLVATODA	420	
Db	361	VLDRECKVEGILEIFDMLLATTSPRELKLOHKEVLCUKAMILLNSSMYPLASANQEA	420	
Qy	421	DSSKLAHLNNAVTDALVWVIKSGISQQOSMELANLLMLLSHVHASNKGMEHLNKM	480	
Db	421	ESSKLTLLNNAVTDALVWVIKSGISQQOSVRLANLLMLLSHVHASNKGMEHLNKM	480	
Qy	481	CKNVVPVYDLLEMLNAHVLRGCKSGITGSECSPAEDSKSGSQNPQSQ	530	
Db	481	CKNVVPVYDLLEMLNAHVLRGCKSGITGSECSSTEDSKNKSQNLQSQ	530	
RESULT 4				
ESR2 MOUSE				
ID	ESR2_MOUSE	STANDARD;	PRT;	530 AA.
AC	O08537;	O35635;	O70519;	
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Estrogen receptor beta (ER-beta).			
GN	ESR2 OR NR3A2 OR ESRB.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_taxid=10090;			
RN	[1]			
RP	SEQUENCE OF 46-530 FROM N.A., AND MUTAGENESIS.			
RC	STRAIN=129/Sv; TISSUE=Ovary;			

RA MEDLINE=97211383; PubMed=9058381;  
 RA Tremblay G.B., Tremblay A., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Labrie P., Giguere V.,  
 RT "Cloning, chromosomal localization, and functional analysis of the  
 RT murine estrogen receptor beta";  
 RL Mol. Endocrinol. 11:353-365(1997).  
 RN [2]  
 RN SEQUENCE OF 46-530 FROM N.A., AND CHARACTERIZATION.  
 RP TISSUE=Ovary;  
 RC MEDLINE=97424142; PubMed=9280064;  
 RX Pettersson K., Grandien K., Kuiper G.G.J.M., Gustafsson J.-A.;  
 RA "Mouse estrogen receptor beta forms estrogen response element-binding  
 RT heterodimers with estrogen receptor alpha";  
 RL Mol. Endocrinol. 11:1486-1496(1997).  
 RN [3]  
 RN SEQUENCE OF 1-60 FROM N.A.  
 RP TISSUE=Ovary;  
 RC Leygue E., Lu B., Dotzlaw H., Glor C., Watson P.H., Murphy L.C.;  
 RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RN SEQUENCE OF 1-60 FROM N.A.  
 RP STRAIN=C57BL/6J X 129; TISSUE=Ovary;  
 RC Rosenfeld C.S., Lubahn D.B.;  
 RX Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN CARBOHYDRATE-LINKAGE SITE SER-61, AND PHOSPHORYLATION SITE SER-61.  
 RP MEDLINE=20450734; PubMed=10995228;  
 RX Cheng X., Cole R.N., Zala J., Hart G.W.;  
 RA "Alternative O-glycosylation/O-phosphorylation of the murine estrogen  
 RT receptor beta";  
 RL Biochemistry 39:11609-11620(2000).  
 RN [6]  
 RN ALTERNATIVE SPLICING.  
 RP TISSUE=Ovary;  
 RC MEDLINE=98348389; PubMed=9685228;  
 RX Lu B., Leygue E., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H.;  
 RA "Estrogen receptor-beta mRNA variants in human and murine tissues";  
 RL Mol. Cell. Endocrinol. 138:199-203(1998).  
 RN [7]  
 RN TISSUE SPECIFICITY.  
 RP MEDLINE=98268825; PubMed=9607809;  
 RX Rosenfeld C.S., Ganjan V.K., Taylor J.A., Yuan X., Stiehr J.R.,  
 RA Hardy M.P., Lubahn D.B.;  
 RT "Transcription and translation of estrogen receptor-beta in the male  
 RT reproductive tract of estrogen receptor-alpha knock-out and wild-type  
 RL mice";  
 RL Endocrinology 139:2982-2987(1998).  
 RN [8]  
 RN INTERACTION WITH NCOA3.  
 RP MEDLINE=97336097; PubMed=9132892;  
 RX Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,  
 RA Rosenfeld M.G.;  
 RT "The transcriptional co-activator p/CIP binds CBP and mediates  
 RT nuclear-receptor function";  
 RL Nature 387:677-684(1997).  
 RN [9]  
 RN INTERACTION WITH NCOA6.  
 RP MEDLINE=20250907; PubMed=10788465;  
 RX Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,  
 RA Reddy J.K.;  
 RT "Isolation and characterization of peroxisome proliferator-activated  
 RT receptor (PPAR) interacting protein (PRIP) as a coactivator for  
 RL PPAR";  
 RL J. Biol. Chem. 275:13510-13516(2000).  
 CC -I- FUNCTION: Nuclear hormone receptor. Binds estrogens with an  
 CC affinity similar to that of ESR1 (ER-alpha), and activates  
 CC expression of reporter genes containing estrogen response elements  
 CC (ERE) in an estrogen-dependent manner. May play a role in ovarian  
 CC follicular growth and maturation.  
 CC -I- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
 CC ESR1. Interacts with NCOA3 and NCOA6 coactivators, leading to a  
 CC strong increase of transcription of target genes. Also interacts  
 CC with NCOA5 (By similarity).



GN ESR2 OR NR3A2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=Holstein; TISSUE=Ovarian follicle;  
RX MEDLINE=99150136; PubMed=10026117;  
RA Rosenfeld C.S., Yuan X., Manikkam M., Calder M.D., Garverick H.A.,  
RA Lubahn D.B.;  
RT "Cloning, sequencing, and localization of bovine estrogen receptor-  
RT beta within the ovarian follicle.";  
RL Biol. Reprod. 60:691-697(1999).  
RN [2]  
RP SEQUENCE OF 4-527 FROM N.A.  
RX MEDLINE=99359179; PubMed=10432221;  
RA Walther N., Lioutas C., Tillmann G., Ivell R.;  
RT "Cloning of bovine estrogen receptor beta (Erbeta): expression of  
RT novel deleted isoforms in reproductive tissues.";  
RL Mol. Cell. Endocrinol. 152:37-45(1999).  
CC -i- FUNCTION: Nuclear hormone receptor. Binds estrogens with an  
CC affinity similar to that of ESR1 (ER-alpha), and activates  
CC expression of reporter genes containing estrogen response elements  
CC (ERE) in an estrogen-dependent manner. May play a role in ovarian  
CC follicular growth and maturation.  
CC -i- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
CC ESR1. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading  
CC to a strong increase of transcription of target genes (By  
CC similarity).  
CC -i- SUBCELLULAR LOCATION: Nuclear.  
CC -i- TISSUE SPECIFICITY: Present in granulosa cells of antral follicles  
CC in various stages of follicular growth.  
CC -i- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
CC a DNA-binding domain and a C-terminal steroid-binding domain.  
CC -i- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
CC subfamily.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF110402; AAC24432.1; -.  
CC EMBL; Y18017; CAB53861.1; ALT\_INIT.  
CC HSP; P03372; IHCQ.  
CC GO; GO:0005634; C:nucleus; ISS.  
CC GO; GO:0003284; P:estrogen receptor activity; ISS.  
CC GO; GO:0004879; P:ligand-dependent nuclear receptor activity; ISS.  
CC GO; GO:0048019; P:receptor antagonist activity; ISS.  
CC GO; GO:0005496; P:steroid binding; ISS.  
CC GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.  
CC GO; GO:0030308; P:negative regulation of cell growth; ISS.  
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
CC InterPro; IPR000536; Hormone\_rec\_lig.  
CC InterPro; IPR001723; Ster\_hrmn\_receptor.  
CC InterPro; IPR008946; Str\_ncl\_receptor.  
CC InterPro; IPR001628; Znf\_C4steroid.  
CC Pfam; PF00104; hormone\_rec; 1.  
CC Pfam; PF00105; zf-C4; 1.  
CC PRINTS; PR00398; STERHORMONER.  
CC PRODOM; PD000035; Znf\_C4steroid; 1.  
CC SMART; SM00430; HOL1; 1.  
CC SMART; SM00399; Znf\_C4; 1.  
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
CC K1 Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
CC Zinc-finger; Steroid-binding; Phosphorylation.  
CC DOMAIN 1 145 MODULATING.

FT DNA BIND 146 211 NUCLEAR RECEPTOR-TYPE.  
FT ZN\_FING 146 166 C4-TYPE.  
FT ZN\_FING 182 206 C4-TYPE.  
FT DOMAIN 212 527 STEROID-BINDING.  
FT MOD\_RES 84 84 PHOSPHORYLATION (BY SIMILARITY).  
FT MOD\_RES 485 485 PHOSPHORYLATION (BY SIMILARITY).  
FT CONFLICT 60 60 N -> D (IN REF. 2).  
SQ SEQUENCE 527 AA; 59031 MW; 9CEFF6106F4E4C84 CRC64;  
Query Match 87.8%; Score 2463.5; DB 1; Length 527;  
Best Local Similarity 87.9%; Pred. No. 6.6e-188;  
Matches 466; Conservative 22; Mismatches 39; Indels 3; Gaps 1;  
QY 1 MDVKSPPSLNSPSSNCQSILPLEHGSIIYIPSSVDSHHEYPAMTFYSPAMVYSIFS 60  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 1 MDVKSPPSLNSPSSNCQSILPLEHGSIIYIPSSVDSHHEYPAMTFYSPAMVYSIFS 60  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 NVTNLGGPGROTTSFNVLPWTPFGHLSPLAVHRLQSHLYABPKSPWCSEARSLEHTLPVN 120  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 ---NSEDGPGRTTTFNVLPWTPFGHLSPLAHCQPSVLYAEQKSPWRETRSLHTLPVN 117  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 121 RETLKRKVGSGNCASPVVTGSGKRDHFCVAGCDSDVAGSHYGVWSCGCKAFKRSIQGH 180  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 118 RETLKRKASGSSCASPSATSPSSKRDHFCVAGCDSDVAGSHYGVWSCGCKAFKRSIQGH 177  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 181 NDYICPATNOCTIDKNRKSQACRLKCYEYGVWKGSRRCRGVLYVRRORSADQLH 240  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 178 NDYICPATNOCTIDKNRKSQACRLKCYEYGVWKGSRRCRGVLYVRRORSADQLH 237  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 241 CAGKAKRSGGHAPRVRELLDLSPEQLVLTLEAPPHVLISRPSPAPTEASMMMLTK 300  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 238 CLSKTRNGPMPTRVKELLSALSPEQLVLTLEAPPHVLISRPSPAPTEASMMMLTK 297  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 301 LADKELVEMISWAKIPGVFELSDFDVRLLSCEMVEVLMGLMRSIDHPGKLIAPDL 360  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 298 LADKELVEMISWAKIPGVFELSDFDVRLLSCEMVEVLMGLMRSIDHPGKLIAPDL 357  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 361 VLDRDEGCKVEGILETFDMLLATTSRFRELQHKYELCVKAMILNLSMYPLVLTATDA 420  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 358 ILDRDEGCKVEGILETFDMLLATTSRFRELQHKYELCVKAMILNLSMYPSATAPQA 417  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 421 DSSRLAHLNNAVTDALVWVIKSGISSQQSQMRANLLMLLSHVHASKGHEHLNKK 480  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 418 DSGRLTLHLNNAVTDALVWVIKSGISSQQSQMRANLLMLLSHVHASKGHEHLNKK 477  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 481 CKNVVPVYDILLEMLNAHLRGCKSITGSECSPAEDSKSKEGSONPQSQ 530  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 478 CKNVVPVYDILLEMLNAHLRGCKSITGSECSPAEDSKSKEGSONPQSQ 527  
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

## RESULT 6

ESR2 SHREP STANDARD; PRT; 527 AA.  
ID \_SR2 SHREP STANDARD; PRT; 527 AA.  
AC Q9TUJ5; Q9N0T6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Estrogen receptor beta (ER-beta).  
GN ESR2 OR NR3A2.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RN SEQUENCE FROM N.A. (ISOFORMS BETA AND BETA-1).  
RC TISSUE=Ovary;  
RX MEDLINE=2131342; PubMed=11420232;  
RA Cardenas H., Burke K.A., Bigsby R.M., Pope W.F., Nephew K.P.;  
RT "Estrogen receptor beta in the sheep ovary during the estrous cycle  
RT and early pregnancy.";  
RL Biol. Reprod. 65:128-134(2001).  
CC -i- FUNCTION: Nuclear hormone receptor. Binds estrogens with an









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DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Stdhmn receptor.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 25 173 MODULATING.
FT DNAS BIND 174 239 NUCLEAR RECEPTOR-TYPE.
FT ZN FING 174 194 C4-TYPE.
FT ZN FING 210 234 C4-TYPE.
FT DOMAIN 240 554 STEROID-BINDING.
SQ SEQUENCE 554 AA; 62173 MW; EC13A96ICEB59C9 CRC64;

Query Match 74.9%; Score 2101; DB 1; Length 554;
Best local Similarity 74.8%; Pred. No. 4.2e-159;
Matches 397; Conservative 50; Mismatches 80; Indels 4; Gaps 3;

Qy 2 DIKNSPSLSNPSYNGSQSLPLEHGSYIPISSYVDSHHEYPAWYTSYPAWYTSIPSN 61
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 26 EIKNSPAGVISPAPYSCNQSLTAEHSPVYIPSSYMSREHYSYTAFCSPAMVYNIA 85
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 62 VTNEGPGGRTTSPNVLPPTPHGLSLPLVHRLSHLYAPQKSPWCEARSLEHTLPVNR 121
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 86 FGDEPAVAARTSPGALMSAPGHLSPLESCQSLLYAEPQKSLWCEARMEVPLPGSR 145
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 122 ETLKRKSGNRCASPV-TGPOKSDAHFCAVCSYAGSYHYGVWSCGCKAFKRSIOGH 180
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 146 ETLKRKTNGNDCTSPIANNPGSKDAHFCAVCSYAGSYHYGVWSCGCKAFKRSIOGH 205
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 181 NDYICPATNOCTIDNREKSCQALRLKCYEVGVKSGRRCGYLVRQRADQLH 240
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 206 NDYICPATNOCTIDNREKSCQALRLKCYEVGVKSGRRCGYLVRQRADQLH 265
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 241 CAGKAKSGGHAPRVRELLDALSPQLVLTLEAPPHVLSRPSAPPTASMMGLTK 300
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 266 CLGRARRYSEAAATVKEILLTSVSPQVLTLEAPPHVLSRPSAPPTASMMGLTK 325
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 301 LADKELVEMISWAKIPGFVLSLFDVRLLESQWELMGLMWSRSDHFGKLIAPDL 360
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 326 LADKELVEMISWAKIPGFVLSLFDVRLLESQWELMGLMWSRSDHFGKLIAPDL 385
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 361 VLDRDEGKCVGILFIDMLLATTSRFRELKLQKKEYLCKVAMILLANSSMPLVTATQDA 420
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 386 VLDRDEGKCVGILFIDMLLATTSRFRELKLQKKEYLCKVAMILLANSSMPLVTATQDA 443
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 421 DSRKLAHLNATVTLVWVIAKSGISSQQSQSMELANILLSHVHASNKGMEHLNMG 480
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 444 ESNRKLHLLNVVTEALVWVIAKSGISSQQSQSMELANILLSHVHASNKGMEHLNMG 503
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 481 CKNVVVVDLLEMLNANVLRCKSSI-TGSECSPAEDSKSGEQSNPQSQ 530
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Qy 504 CKNVVVVDLLEMLNANVLRCKSLATHPFGPELQMEPCESLRKGEPQ 554
Db :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 9
ESR2_COTJA
ID ESR2_COTJA STANDARD; PRT; 472 AA.
AC O93511
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
RN [1]_SEQUENCE FROM N.A.
RA Foidart A., Lakaye B., Grisar T., Bail G.P., Balthazart J.;
RT "Sequence and neuroanatomical distribution of estrogen receptor beta
in the quail brain.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 141-286 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98430913; PubMed=9760113;
RA Lakaye B., Foidart A., Grisar T., Balthazart J.;
RT "Partial cloning and distribution of estrogen receptor beta in the
avian brain.";
RL NeuroReport 9:2743-2748(1998).
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: A HIGH EXPRESSION IS SEEN IN THE
TELENCEPHALON, DIENCEPHALON, PITUITARY, TESTIS AND KIDNEYS BUT
LITTLE OR NO EXPRESSION IS SEEN IN THE CEREBELLUM, PECTORAL MUSCLE
AND ADRENAL GLAND.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
subfamily.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licenses@isb-sib.ch)
CC -----
DR EMBL; AF045149; AAC36463.2; --
DR HSP; P03372; hRCQ.
DR GO; GO:0005634; Cnucleus; ISS.
DR GO; GO:0030284; P:estrogen receptor activity; ISS.
DR GO; GO:0004879; P:ligand-dependent nuclear receptor activity; ISS.
DR GO; GO:0048019; P:receptor antagonist activity; ISS.
DR GO; GO:0005496; F:steroid binding; ISS.
DR GO; GO:0005200; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0030308; P:negative regulation of cell growth; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Stdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 104 MODULATING.
FT DNAS BIND 105 170 NUCLEAR RECEPTOR-TYPE.
FT ZN FING 105 125 C4-TYPE.
FT ZN FING 141 165 C4-TYPE.
FT DOMAIN 171 472 STEROID-BINDING.
SQ SEQUENCE 472 AA; 53411 MW; DF7A78F0FDBD188D CRC64;

Query Match 69.8%; Score 1959; DB 1; Length 472;
Best local Similarity 80.1%; Pred. No. 6.4e-148;
```

Matches 370; Conservative 39; Mismatches 47; Indels 6; Gaps 3;  
QY 46 MTFYSPAVNYSIPSNVNLGGPGRTTSPNVLPWTPGHLSPVLVHROLSHLYAEPQKS 105  
DB 1 MAFCSFAMNNTYASNFSGSASVRSQTSPSLWAPGHLSPVLTHCQLSLLYAEPQKS 60  
QY 106 PWCEARSLEHTLPVNRRETLKRVSGNRCASPV-TGPGSKRDAHFCAVCSYDASGYHYGVW 164  
DB 61 PWCEARPLPVLVPSRETLKRTKNGSDCTSPASNFGSKRDAHFCAVCSYDASGYHYGVW 120  
QY 165 SCEGKAPFRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVMKGSRRRC 224  
DB 121 SCEGKAPFRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVMKGSRRRC 180  
QY 225 GYELVRRQSSADEQLHCAGKAKSGHAPRVRELLLDALSPVOLVTLLEAPPHVLSR 284  
DB 181 GYELVRRQSSADEQLHCAGKAKSGHAPRVRELLLDALSPVOLVTLLEAPPHVLSR 237  
QY 285 PSAPPTFASMMSLTKLADKELVHMIISWAKKIPGFVELSLFDQVRLLESCHWVEVLMMGLM 344  
DB 238 PSKPPTFASMMSLTKLADKELVHMIISWAKKIPGFIDLSLYDQVRLLESCHWVEVLMMGLM 297  
QY 345 WRSIDHPGKLIAPDLVLDRECKVEGILEIFDMLLATTSRPRELKHQKVEYLCVKAMI 404  
DB 298 WRSIDHPGKLIAPDLVLDRECKVEGILEIFDMLLATTSRPRELKHQKVEYLCVKAMI 357  
QY 405 LNSSMYPLVTATQDADSSRKLHLNNAVTDALVWVIAKSGISSQQSSMRLANLMLLHSH 464  
DB 358 LNSSMFPL--SPEEPESNKLHLNNAVTDALVWVIAKSGIPSQOQTRLANLMLLHSH 415  
QY 465 VHRASNGMEHLNKKCNVVPVYDILLEMLNAHTLRGQRKS 506  
DB 416 VHRASNGMEHLNKKCNVVPVYDILLEMLNAHTLRGQRKS 457

RESULT 10  
ESR2\_CHICK  
ID ESR2\_CHICK STANDARD; PRT; 472 AA.  
AC QPRT05; 2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DB Estrogen receptor beta (ER-beta) (cERb).  
GN ESR2 OR NR3A2.  
OS Gallus gallus (Chicken).  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White leghorn; TISSUE=Testis;  
RA Suzuki M., Mizuno S., Nakabayashi C.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF  
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING  
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.  
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-  
ALPHA.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
a DNA-binding domain and a C-terminal steroid-binding domain.  
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
subfamily.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC

EMBL; AB036415; BAA88667.1; -.  
HSP; P03372; LHQ.  
DR InterPro; IPR000516; Hormone\_rec\_lig.  
DR InterPro; IPR001723; Stdhmm\_receptor.  
DR InterPro; IPR008446; Std\_ncl\_receptor.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf\_C4; 1.  
DR PRINTS; PR00398; STRODHOMER.  
DR PRINTS; PR00047; STROIDFINGER.  
DR ProDom; PD000035; Znf\_C4steroid; 1.  
DR SMART; SM00430; HOL1\_1.  
DR SMART; SM00399; Znf\_C4; 1.  
DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
KW Zinc-finger; Steroid-binding.  
FT DOMAIN 1 104 MODULATING.  
FT DNA\_BIND 105 170 NUCLEAR RECEPTOR-TYPE.  
FT ZN\_FING 105 125 C4-TYPE.  
FT ZN\_FING 141 165 C4-TYPE.  
FT DOMAIN 171 472 STEROID-BINDING.  
SQ SEQUENCE 472 AA; 53439 MW; ABCBB88CACA65650 CRC64;  
Query Match 69.5%; Score 1948.5; DB 1; Length 472;  
Best Local Similarity 79.3%; Pred. No. 4,4e-147;  
Matches 371; Conservative 38; Mismatches 52; Indels 7; Gaps 4;  
QY 46 MTFYSPAVNYSIPSNVNLGGPGRTTSPNVLPWTPGHLSPVLVHROLSHLYAEPQKS 105  
DB 1 MAFCSFAMNNTYASNFSGSASVRSQTSPSLWAPGHLSPVLTHCQLSLLYAEPQKS 60  
QY 106 PWCEARSLEHTLPVNRRETLKRVSGNRCASPV-TGPGSKRDAHFCAVCSYDASGYHYGVW 164  
DB 61 PWCEARPLPVLVPSRETLKRTKNGSDCTSPASNFGSKRDAHFCAVCSYDASGYHYGVW 120  
QY 165 SCEGKAPFRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVMKGSRRRC 224  
DB 121 SCEGKAPFRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVMKGSRRRC 180  
QY 225 GYELVRRQSSADEQLHCAGKAKSGHAPRVRELLLDALSPVOLVTLLEAPPHVLSR 284  
DB 181 GYELVRRQSSADEQLHCAGKAKSGHAPRVRELLLDALSPVOLVTLLEAPPHVLSR 237  
QY 285 PSAPPTFASMMSLTKLADKELVHMIISWAKKIPGFVELSLFDQVRLLESCHWVEVLMMGLM 344  
DB 238 PSKPPTFASMMSLTKLADKELVHMIISWAKKIPGFIDLSLYDQVRLLESCHWVEVLMMGLM 297  
QY 345 WRSIDHPGKLIAPDLVLDRECKVEGILEIFDMLLATTSRPRELKHQKVEYLCVKAMI 404  
DB 298 WRSIDHPGKLIAPDLVLDRECKVEGILEIFDMLLATTSRPRELKHQKVEYLCVKAMI 357  
QY 405 LNSSMYPLVTATQDADSSRKLHLNNAVTDALVWVIAKSGISSQQSSMRLANLMLLHSH 464  
DB 358 LNSSMFPL--SPEEPESNKLHLNNAVTDALVWVIAKSGIPSQOQTRLANLMLLHSH 415  
QY 465 VHRASNGMEHLNKKCNVVPVYDILLEMLNAHTLRGQRKS 511  
DB 416 VHRASNGMEHLNKKCNVVPVYDILLEMLNAHTLRGQRKS 463

RESULT 11  
ESR2\_ANGJA  
ID ESR2\_ANGJA STANDARD; PRT; 573 AA.  
AC O13012;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Estrogen receptor beta (ER-beta).  
GN ESR2 OR NR3A2.  
OS Anguilla japonica (Japanese eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla.

```

NCBI_TaxID=7937;
[1]
RN RN
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=96386022; PubMed=8793852;
Todo T. Adachi S., Yamauchi K.;
RA "Molecular cloning and characterization of Japanese eel estrogen
RT receptor cDNA.";
RL Mol. Cell. Endocrinol. 119:37-45(1996).
CC !- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC !- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CC ALPHA.
CC !- SUBCELLULAR LOCATION: Nuclear.
CC !- TISSUE SPECIFICITY: Liver.
CC !- INDUCTION: By 17-Beta-estradiol.
CC !- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC !- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB003356; BAA19851.1; -
DR HSP; P03372; IHCO.
DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:00030284; P:steroid receptor activity; ISS.
DR GO; GO:0004879; P:ligand-dependent nuclear receptor activity; ISS.
DR GO; GO:00048019; P:receptor antagonist activity; ISS.
DR GO; GO:0005496; P:steroid binding; ISS.
DR GO; GO:00030520; P:steroid receptor signaling pathway; ISS.
DR GO; GO:0030308; P:negative regulation of cell growth; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Sterhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDPFINGER.
DR Prodom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR KMW RECEPTOR; Transcription regulation; DNA-binding; Nuclear protein;
DR Zinc-finger; Steroid-binding.
FT DOMAIN 15 170 MODULATING.
FT DNA_BIND 171 236 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 171 191 C4-TYPE.
FT ZN_FING 207 231 C4-TYPE.
FT DOMAIN 237 573 STEROID-BINDING.
SQ SEQUENCE 573 AA; 63420 MW; 9C64C1D8D39ED4CC CRC64;
Query Match 55.2%; Score 1549; DB 1; Length 573;
Best Local Similarity 57.7%; Pred. No. 3e-115;
Matches 313; Conservative
Cy 13 PSSVNCQSQTILPLEHGSIIYIPSSIVDSHHEYPAMTFYSPVAMVYSIPNVNLEGCP----69
Db 33 PTMYNGALPALSMESHAVCIIPSYPTDSDSHYAALTFFYSPFLSH-----GGPAMP 82
Qy 70 ---GRTTTPNVNLWPT---PGLHSLPLVVRHQLSHLYAEPOKSPWCSEARSLEHTLPVNR 122
Db 83 ESPAPRQSLSPSLFWPAHGHHGHVSPALHPHQQLPVVREPAHSPWASPKPLEH-----GQ 137

```

QY	123	TLRKVSVGRCAVSPVTPGRGS-----KRDHFCAVCSDVASGVHYGVWSCGCKKAPFKR	197
DB	138	AQTSKLAKGRKMASSSEETSSVGGCPAGKGDWHFCVCHDYASGTHYGVWSCGCKKAPFKR	197
QY	176	SIQGHNDYICPATNQCTIDKNRKAQCLRLKCYEYGMVKGSRRRRCGYRLVRRQSA	235
DB	198	SIQGHNGYICPATNQCTIDKNRKAQCLRLKCYEYGMVKGSRRRRCGYRLVRRQSA	257
QY	236	D--EQLHCAGKA--KRSQGHAPRVRELLDALSPQVLTLLEAEPPHV-LISRPSAPP	289
DB	258	HIRELAGTGGGARTQRGEGVVFQTQBAQSALTPSQLINRIIEAPEIYLMKELKXPP	317
QY	290	TEASMMMSLTKLADKELVHMSWAKKIPGFVLSLFDQVRLLESQWNEVLMGLMWSRID	349
DB	318	TEDSMMMSLTNLADKELVHMSWAKKIPGFVSLDLSQVHLLBCQLEVLMLGLMWSVD	377
QY	350	HPGKLIAPDLVLDRRGKCVGEGILETFDMLLATTSFRELKIQHEKVELCVKAMILLNS	409
DB	378	HPGKLIAPDLVLDRRGKCVGEGILETFDMLLATTSFRELKIQHEKVELCVKAMILLNS	437
QY	410	MYPLVTAT-QDADSSRKLAHLNAVTDALVWVIAKSGISSQQQNMRLNMLMLSHVTHA	468
DB	438	LCATTSSENRELESRNKLHMLDVSVDALVWVIAKSGISSQQQNMRLNMLMLSHVTHA	497
QY	469	SNKGMEHLNWKCNVVPVVDLLEMLNAHVLGRCKSSITGSECSAPDSDSKSKEGQNPQ	528
DB	498	SNKGMEHLNWKCNVVPVVDLLEMLNAHVLGRCKSSITGSECSAPDSDSKSKEGQNPQ	550
QY	529	SQ 530	
DB	551	SQ 552	

RESULT 12

ERBI\_CARAU

AC

Q9W669;

ID

ERBI\_CARAU

STANDARD;

PRF;

568 AA.

DT

16-OCT-2001

(Rel. 40, Created)

DT

16-OCT-2001

(Rel. 40, last sequence update)

DT

28-FEB-2003

(Rel. 41, last annotation update)

DE

Batrogen receptor beta-1 (ER-beta-1).

OS

Carassius auratus (Goldfish).

OC

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC

Cyprinidae; Carassius.

OX

NCBI\_TaxID=7957;

[1]

SEQUENCE FROM N.A.

RP

TISSUE=Liver;

RC

MEDLINE=99169117; PubMed=1068500;

EX

Tchoudakova A.V.; Pathak S.; Callard G.V.;

RA

Molecular cloning of an estrogen receptor beta subtype from the

RT

goldfish, Carassius auratus.;

RL

Gen. Comp. Endocrinol. 113:388-400(1999).

CC

!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF

CC

ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING

CC

ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.

CC

!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-

CC

ALPHA (BY SIMILARITY).

CC

!- SUBCELLULAR LOCATION: Nuclear.

CC

!- DOMAIN: Composed of three domains: a modulating N-terminal domain,

CC

a DNA-binding domain and a C-terminal steroid-binding domain.

CC

!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3

CC

subfamily.

CC

-----

CC

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CC

CC

```
DR EMBL; AF061269; AAD26921.1; -.
DR HSP; P03372; IERR.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 12 169 MODULATING.
FT DNA_BIND 170 235 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 170 190 C4-TYPE.
FT ZN_FING 206 230 C4-TYPE.
FT DOMAIN 236 568 STEROID-BINDING.
SQ SEQUENCE 568 AA; 63539 MW; 2B678D075DB76F9 CRC64;

Query Match 52.3%; Score 1466; DB 1; Length 568;
Best Local Similarity 56.0%; Pred. No. 1.1e-108;
Matches 290; Conservative 75; Mismatches 127; Indels 26; Gaps 10;

Qy 12 SPSSVNCQSITLPLEHGSIVIPSSVVDSHHEYPAWTFVSPAVMNYSPSNVNLGGPG- 70
Db 38 SP-FNSSSSPLVESHPCIPSPYDGLGHDTFTLPFYSPLLGY----GTSPLSDCPV 92

Qy 71 RQTSPNVLNPTPGHLSPLVVRQLSHLYA-EPOKSPWCEARSLEHTLPVNRRTLRKVS 129
Db 93 RQSLSPFLFWPPHSHVSSSLALHQQOTRLQPNHPTGGTWAELTPHDHCEENCKPLSKRVA 152

Qy 130 GNRCASTPGSGTRDAHPCAVCSYAGSHYGVWCEGCKAPFKRSIQGHNDVICPATN 189
Db 153 VAETS--TSLRGKADMEHYCAVCSYAGSHYGVWCEGCKAPFKRSIQGHNDVICPATN 210

Qy 190 QCTIDKRRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAXR 247
Db 211 QCTIDKRRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAXR 266

Qy 248 SGHAPVR-----ELLDLSPQLVLTLEAPPRIV-LISPSAPFTASMMMS 297
Db 267 SGPRSQEKTVQRPLSGNKVVTALSPBELIARINDAEPPEIYLMKDYKXFTFTEANVMS 326

Qy 298 LTKLADKELVEMISWAKKIPGVFVLSLFDQVRLLESQWMEVLMGLMWSIDHPGLKIFA 357
Db 327 LTNLADKELVEMISWAKKIPGVFVLSLFDQVRLLESQWMEVLMGLMWSIDHPGLKIFA 386

Qy 358 PDLVLDREKCVEGILEIFDMLLATTFRFRELKLOHKEYLCVKAMILLNSM-YPLVTA 416
Db 387 PDLVLDREKCVEGILEIFDMLLATTFRFRELKLOHKEYLCVKAMILLNSM-YPLVTA 446

Qy 417 TQDADSSRLAHLLNAVTDALVWYAKSGISSQQSQSMELANLLMLSHVRHASKNGMEHL 476
Db 447 GEELQSRSKLCLLDVSDVDAFWAISKTLGSPQORSTKLALLMLSHVRHASKNGMEHL 506

Qy 477 LNAKCKNVPVYVLDLLEMLNARVLRGCKSSITGSECS 514
Db 507 HSMKMKQAVPYLDLLEMLNARVLRGCKSSITGSECS 544

RESULT 13
ESR2 ONCMY STANDARD; PRT; 568 AA.
AC P57782;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2.
```

```
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Haug M., Ackermann G., Pent K.;
RT "Molecular cloning of an estrogen receptor beta subtype from rainbow trout.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CC ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AJ289883; CAC06714.1; -.
CC HSP; P03372; IERR.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Steroid_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 177 MODULATING.
FT DNA_BIND 178 243 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 178 198 C4-TYPE.
FT ZN_FING 214 238 C4-TYPE.
FT DOMAIN 244 568 STEROID-BINDING.
SQ SEQUENCE 568 AA; 63813 MW; F7A7BD7B3B2C2804 CRC64;

Query Match 51.4%; Score 1440.5; DB 1; Length 568;
Best Local Similarity 54.9%; Pred. No. 1.2e-106;
Matches 289; Conservative 85; Mismatches 121; Indels 31; Gaps 11;

Qy 16 YNCQSITLPLEHGSIVIPSSVVDSHHEYPAWTFVSPAVMNY-SIPSNVNLGGPGRQTT 74
Db 49 FNSSSSPLVESHPCIPSPYDGLGHDTFTLPFYSPALLGYGTSPLS----ECSVQSL 104

Qy 75 SPNVLNPTPGHLSPLVVRQLSHLYA-EPOKSPWCEARSLEHTLPVNRRTLRKVSNGRC 133
Db 105 SPTLFWPPHSHVSSSLALHQQOTRLQPNHPTGGTWAELTPHDHSEEBYRKPLVRRVADAE 164

Qy 134 ASPVTGPGSKEDAHFCAVCSYAGSHYGVWCEGCKAPFKRSIQGHNDVICPATNCTI 193
Db 165 TS--TSLRGKADMEHYCAVCSYAGSHYGVWCEGCKAPFKRSIQGHNDVICPATNCTI 222

Qy 194 DKNRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAKRSGGH 251
Db 223 DKNRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAKRSGGH 278
```

```

QY 252 APRVR-----ELLDAISPEOLVITLEAEPHV-LISRPAPFTEASMMVSLTKL 301
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 279 SOEMKSVCPCLSGNEVWVNMALTPBELIARIMDAEPPEIYLMKDKMCKPTEANVMSLTNL 338
QY 302 ADKELVHMISNAKKIPGVFVLSLPDQVLLSCWMEVLMGLMWSIDHPCKLIFAPDLY 361
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 339 ADKELVHMISNAKKIPGVFVLSLPDQVLLSCWMEVLMGLMWSVNHPPKLIFFPDLS 398
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 362 LDRDEGKCVGEILEIFDMLATTFRFELKQHKYLCVKAMILNNSMYPVLTATODAD 421
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 399 LSRDEGSCVQGVFEIYFDMLAATSRFELKQREYVCLKAMILNNSM--CLSSSEGG 456
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 SSR---KLANHLNATVLDALVWIAKSGISSQOQNRLANLMLSHVHRASNGWEHLN 478
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 457 ELQRRSKLLDSVTDALVWIAKSGISSQOQNRLANLMLSHVHRASNGWEHLN 516
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 479 MKCKNVVFPYDILLENLAHNAHVLRGKSSITGSECSPAEDSKSKEGS 524
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 517 MKCKNVVFPYDILLENLAHNAHVLRGKSSITGSECSPAEDSKSKEGS 560
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
ESR2 MICUN STANDARD; PRT; 673 AA.
ID ESR2 MICUN STANDARD; PRT; 673 AA.
AC P57781;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2.
OS Micropogonias undulatus (Atlantic croaker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sciaenidae; Micropogonias.
OX NCBI_taxid=29154;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461442; PubMed=11005855;
RA Hawkins M.B., Thornton J.W., Crews D., Skipper J.K., Dotte A.,
RA Thomas P.,
RT Identification of a third distinct estrogen receptor and
RT reclassification of estrogen receptors in teleosts";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10751-10756(2000).
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CC ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: ABUNDANT IN THE LIVER AND TESTES, LESS
CC ABUNDANT IN THE OVARY AND BARELY DETECTABLE IN THE MUSCLE.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF298181; AAC16711.1; -.
CC HSSP; P03372; 1HCO.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Stchrnm_receptor.
CC InterPro; IPR008946; Strncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.

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DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PDG00035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 181
FT DNABIND 182 247
FT ZNFING 182 202
FT ZNFING 218 242
FT ZNFING 248 253
FT DOMAIN 248 653
FT STERIOD-BINDING.
SQ SEQUENCE 673 AA; 74680 MW; 2839451577E3D01 CRC64;

Query Match 51.0%; Score 1431; DB 1; Length 673;
Best Local Similarity 53.5%; Pred. No. 8.5e-106;
Matches 303; Conservative 76; Mismatches 125; Indels 62; Gaps 18;

QY 6 SPSSLSNPSVNCQSITLPLEHGSIVIPSSVYDSHHEY-----PAMTEYSVAVNMYSPSN 61
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 31 SPGLL--PAVYS---PPLGMDSHVCLIPSPYTOSSHEYNHSHGHLPTIFYSVLSYRPP- 84
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VTNLEGGPGR--QVTSFNVLMPTFGH--LSPLVHRQLSHLYABPQ-KSPWCEAR----- 111
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 85 ITN---SPSSILCPSLSPSAFMPSHNPTMPSLTLCPEFISIVYNPSHPAFWLESKAHSIN 141
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 112 -SLEHTLPVNRETLKRKVG-----NRCAFPYTGSGKEDAFCAVCSYASGYHYGVW 164
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 142 ASSSSIGCNKSLVYKRSSEGVEDMNSLCSAV-----GKADMFCAVCHDYASYHYGVW 197
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 SCBGKAPFFKRSIQGHNDYICPATNOCITDKNRKSCQACRLRKYEVGMVKCGSRERC 224
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 198 SCBGKAPFFKRSIQGHNDYICPATNOCITDKNRKSCQACRLRKYEVGMVKCGVRERC 257
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 225 GYRLVRRQRS-----ADEQLHCAGKAKRSGGH-----AP-RVRELLLDLSP 265
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 258 SYRGARHRRGGLQFRDPTGRGLVRVGLGSAQSHLLEAPLTPLAPLQAKHVLSSMSP 317
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 266 EQVLVTLLEAPPHV-LISRPSAPFTEASMMSLTKLADKELVHMISNAKKIPGVFVLSL 324
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 318 EEFISRIMDAEPPEIYLMEDLKKEPTEASMMSLTKLADKELVHMISNAKKIPGVFVLSL 377
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 325 FDQVRLLESQWELVLMGLMWSRIDHPCKLIFAPDLYLDRDEGKCVGEILEIFDMLATT 384
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 378 ADQINILKCCWLEILMLGLMWSVDHPCKLIFSPDFKLNREEGQCVGEIMEIFDMLLAGT 437
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 385 SRREELKQHKYLCVKAMILNNSMYPVLTAT-QQADSSRKLHLNATVLDALVWIAK 443
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 438 SRREELKQHKYLCVKAMILNNSMYPVLTAT-QQADSSRKLHLNATVLDALVWIAK 497
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 444 SGISSQOQNRLANLMLSHVHRASNGWEHLNNAHVLRGKSSITGSECSPAEDSKSKEGS 503
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 498 MGLTTOQTUQLGLTLGLSHIRSVNKGMDHLSTWKRKNVVLVYDILLENLAHNAHVL 556
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 504 KSITGSECSPAEDSKS-KEGSONPQ 528
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 557 -----GSPSSSPSSSETYSQHQYTPQ 577
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ESR2 MACMU
ID ESR2 MACMU STANDARD; PRT; 279 AA.
AC Q9TIE5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Estrogen receptor beta (ER-beta) (Fragment).
GN ESR2 OR NR3A2
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rutheria; Primates; Catarrhini; Cercopithecoidea;

```

OC Cercopithecinae; Macaca.  
OX NCBI\_taxid=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20113291; PubMed=10644527;  
RA Wu X.H., Ma X.H., Smith G.C.S., Nathanielsz P.W.;  
RF "Differential distribution of ERalpha and ERbeta mRNA in intrauterine  
RT tissues of the pregnant rhesus monkey.";  
RL Am. J. Physiol. 278:C190-C198(2000).  
CC -!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an  
CC affinity similar to that of ER1 (ER-alpha), and activates  
CC expression of reporter genes containing estrogen response elements  
CC (ERE) in an estrogen-dependent manner. May play a role in ovarian  
CC follicular growth and maturation.  
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
CC ESR1. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading  
CC to a strong increase of transcription of target genes (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
CC a DNA-binding domain and a C-terminal steroid-binding domain.  
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
CC subfamily.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: AF119229; AAD54069.1; --  
DR HSSP: P03372; 1ERR.  
DR InterPro: IPR000536; Hormone\_rec\_lig.  
DR InterPro: IPR001723; Steroid\_receptor.  
DR InterPro: IPR008946; Str\_ncl\_receptor.  
DR InterPro: IPR001628; Znf\_C4steroid.  
DR Pfam: PF00104; hormone\_rec; 1.  
DR PRINTS: PR00398; STRDHORMONER.  
DR SMART: SM00430; HOL1; 1.  
DR PROSITE: PS00031; NUCLEAR RECEPTOR; PARTIAL.  
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
KW Zinc-finger; Steroid-binding; Phosphorylation.  
FT NON\_TER 1  
FT DOMAIN <1> 279 STEROID-BINDING.  
FT MOD\_RES 251 251 PHOSPHORYLATION (BY SIMILARITY).  
FT NON\_TER 279 279  
SQ SEQUENCE 279 AA; 858D9B7D01DA0301 CRC64;  
  
Query Match 49.8%; Score 1398; DB 1; Length 279;  
Best Local Similarity 98.2%; Pred. No. 1.1e-103;  
Matches 274; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 238 QLHCAGKAKRSGHAPVRELLLDALSPQLVLTLEAAPPVHLISRPSPAPTEASMMMS 297  
Db 1 QLHCAGKAKRSGHAPVRELLLDALSPQLVLTLEAAPPVHLISRPSPAPTEASMMMS 60  
  
QY 298 LTKLADKELVHMISWAKKIPGFVLSLFDQVRLLESQWNEVLMVGLMWSIDHPGKLI 357  
Db 61 LTKLADKELVHMISWAKKIPGFVLSLFDQVRLLESQWNEVLMVGLMWSIDHPGKLI 120  
  
QY 358 PDLVLDREKCGVEGLEIFDMLATTSRFREKLQHKYLCVKAMILLNSMYPLVTAT 417  
Db 121 PDLVLDREKCGVEGLEIFDMLATTSRFREKLQHKYLCVKAMILLNSMYPLVTAT 180  
  
QY 418 QDADSSRKLHLINAVTDALVWIAKSGISSQQSQMRLANLLMLLSHVHASNKGMEHLL 477  
Db 181 QDADSSRKLHLINAVTDALVWIAKSGISSQQSQMRLANLLMLLSHVHASNKGMEHLL 240  
  
QY 478 NMKCKRVVPYDILLLEMANHVLRCCKSSITGSECSPAE 516  
Db 241 SMKCKRVVPYDILLLEMANHVLRCCKSSITGSECSPAE 279

Search completed: June 20, 2004, 10:37:40  
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:34:32 ; Search time 46 Seconds  
(without alignments)  
3635.318 Million cell updates/sec

Title: US-08-906-365-2

Perfect score: 2805  
Sequence: 1 MDKNSPSSLSNPPSYNCSQ.....ECSPAEDSKSKEGQNPPQSQ 530

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTEMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2483	88.5	567	11	Q8BG65 mus musculus
2	2420	86.3	499	6	Q5MFO macaca arct
3	2317	82.6	486	6	Q5ME9 callithrix
4	2273	81.0	503	11	Q91286
5	1723	61.4	323	4	Q86231 homo sapien
6	1691	60.3	542	13	Q90286
7	1553	55.4	335	11	Q8CGK9 cavia porce
8	1471.5	52.5	559	13	Q8JUB9 cyprinus ca
9	1455.5	51.9	553	13	Q7ZU32
10	1454.5	51.9	553	13	Q90WS8 brachydanio
11	1441.5	51.4	553	13	Q8AV62
12	1410.5	50.3	565	13	Q8QHK9
13	1409.5	50.2	553	13	Q804Q7 acanthopagr
14	1401	49.9	671	13	Q7T2K7 halichoeres
15	1397.5	49.8	592	13	Q90WS9 brachydanio
16	1396	49.8	601	13	Q7T3U5 candidia ba

17	1389.5	49.5	553	13	Q98SM7
18	1389.5	49.5	592	13	Q98SM8
19	1388.5	49.5	612	13	Q7T3U4 varicorhinu
20	1366	48.7	562	13	Q8UW75
21	1293	44.3	250	6	Q95JC0 canis famil
22	1235.5	44.0	581	13	Q8UWA9
23	1232.5	43.9	589	13	Q8AYH0
24	1216.5	43.4	587	13	Q8UWB0
25	1213	43.2	570	13	Q800Q2
26	1199	42.7	574	13	Q7T2K8
27	1188	42.4	564	13	Q90WV1
28	1180.5	42.1	620	13	Q7SZ10
29	1172.5	41.8	583	13	Q804Q6
30	1166.5	41.6	578	13	Q8QHL0
31	1165.5	41.6	431	6	Q95L13
32	1157	41.2	620	13	Q90WH6
33	1118	39.9	554	13	Q90ZM8
34	1099	39.2	458	13	Q9DDJ3
35	942.5	33.6	335	13	Q9DDZ4
36	900	32.1	208	11	Q8K4S0
37	831.5	29.6	353	11	Q8CGK8
38	679	24.2	276	13	Q91984
39	659	23.5	134	6	Q864V2
40	643	22.9	466	11	Q8CHC9
41	622.5	22.2	433	11	Q8C7A6
42	622.5	22.2	434	11	Q80VSI
43	615.5	21.9	433	11	Q8CCV5
44	594.5	21.2	200	13	Q90ZS9
45	544	19.4	139	11	Q9JMW7

ALIGNMENTS

RESULT 1

Q8BG65 PRELIMINARY; PRT; 567 AA.

AC Q8BG65; 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Estrogen receptor 2.  
GN ESR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Ovary;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The PANTOM Consortium.  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK054290; BAC35770.1; -  
DR EMBL; AK054413; BAC35770.1; -  
DR PIR; PT0649; PT0712.  
DR MGD; MGI:105392; Esr2.  
DR GO; GO:0005496; P:steroid binding; IDA.  
DR GO; GO:0007420; P:brain development; IMP.  
DR GO; GO:0007928; P:cell motility; IMP.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.  
DR InterPro; IPR000536; Hormone rec lig.  
DR InterPro; IPR001723; Sterhmrn receptor.  
DR InterPro; IPR008946; Str\_ncl\_receptor.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00398; STRODHORMNER.  
DR PRINTS; PR00047; STROIDFINGER.  
DR ProDom; PD000035; Znf\_C4steroid; 1.

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DR SMART; SMO0430; HOLI; 1.
DR SMART; SMO0399; Znf C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
SQ SEQUENCE 567 AA; 63217 MW; BFB388C189FABE78 CRC64;

Query Match      88.5%; Score 2483; DB 11; Length 567;
Best Local Similarity 85.8%; Pred. No. 3.4e-219; Indels 18; Gaps 1;
Matches 470; Conservative 25; Mismatches 35;

Qy 1 MDIKNSPSSLSNPSYNSQSIPLHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNSIPS 60
Db 20 MEIKNSPSSLSNPSYNSQSIPLHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNSIPS 79
Qy 61 NVTNLEGGPGROTPSPNVLWTFPGHLSPLVHRLSHLYAEPQKSPWCEARSLEHTLPVN 120
Db 80 STGNLEGGPGROTPSPNVLWTFPGHLSPLVHRLSHLYAEPQKSPWCEARSLEHTLPVN 139
Qy 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGVNSCEGCKAFFKRSIQGH 180
Db 140 RETLKRKLGSGCASPVTPSPAKRDHAFCAVCSYASGYHYGVNSCEGCKAFFKRSIQGH 199
Qy 181 NDYICPATNQCTIDKNRKSCQACRLKCYEYGVNKGSRERCGYLRVRRQSADEQLH 240
Db 200 NDYICPATNQCTIDKNRKSCQACRLKCYEYGVNKGSRERCGYLRVRRQSADEQLH 259
Qy 241 CAGKAKSGGCHAPRVRELLLDALSPQQLVTLLEAEPHVLISRPSPAPFTEASMMMSLTK 300
Db 260 CLNKAKRTSGHTPRVKELLANSLSPEQLVTLLEAEPHVLISRPSPAPFTEASMMMSLTK 319
Qy 301 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 360
Db 320 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 379
Qy 361 VLD-----RDEGKCVGEILEIFDMLLATTTSRRELKQHKYLCVKA 402
Db 380 VLDSSDPHHVAQTSKAVPRDEGKCVGEILEIFDMLLATTTSRRELKQHKYLCVKA 439
Qy 403 MILLNSMYPLVTATQDADSRKLAHLNVAVDALVWVIAKSGISSQQSRLANLML 462
Db 440 MILLNSMYPLATASQEAESRKLTHLLNVAVDALVWVIAKSGISSQQSRLANLML 499
Qy 463 SHVRHSHKNGEHLNKKNVVPVYDILLEMLNAHLVLRGCKSSITSECSPEADSKSE 522
Db 500 SHVRHSHKNGEHLNKKNVVPVYDILLEMLNAHLVLRGCKSSITSECSPEADSKSE 559
Qy 523 GSQNPQSQ 530
Db 560 GSQNLQSQ 567

RESULT 2
Q95MF0
ID Q95MF0 PRELIMINARY; PRT; 499 AA.
AC Q95MF0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Estrogen receptor beta 2.
GN ERBT2A2.
OS Macaca arctoides (Stump-tailed macaque).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OC NCBI_TaxID=9540;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RA Scobie G.A., Wilson J.A., Millar M.R., Macpherson S., Saunders P.T.;
RT "The estrogen receptor beta variant ERBeta cx/ERBeta2 is expressed in
RT a wide range of tissues in both Old and New World primates.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AF393815; AAK71317.1; -.
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DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0048019; F:receptor antagonist activity; ISS.
DR GO; GO:0005496; F:steroid binding; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0030308; P:negative regulation of cell growth; ISS.
DR GO; GO:0006355; P:negative regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STERDORMONER.
DR PRINTS; PR00047; STROIDDFINGER.
DR ProDom; PD0000035; Znf_C4steroid; 1.
DR SMART; SMO0430; HOLI; 1.
DR SMART; SMO0399; Znf C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 499 AA; 55782 MW; A91DA345C8718COA CRC64;

Query Match      86.3%; Score 2420; DB 6; Length 499;
Best Local Similarity 95.6%; Pred. No. 1.7e-213; Indels 0; Gaps 0;
Matches 456; Conservative 6; Mismatches 15;

Qy 1 MDIKNSPSSLSNPSYNSQSIPLHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNSIPS 60
Db 1 MDIKNSPSSLSNPSYNSQSIPLHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNSIPS 60
Qy 61 NVTNLEGGPGROTPSPNVLWTFPGHLSPLVHRLSHLYAEPQKSPWCEARSLEHTLPVN 120
Db 61 NVTNLEGGPGROTPSPNVLWTFPGHLSPLVHRLSHLYAEPQKSPWCEARSLEHTLPVN 120
Qy 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGVNSCEGCKAFFKRSIQGH 180
Db 121 RETLKRKVSNGRCASPVTPSPSKRDHAFCAVCSYASGYHYGVNSCEGCKAFFKRSIQGH 180
Qy 181 NDYICPATNQCTIDKNRKSCQACRLKCYEYGVNKGSRERCGYLRVRRQSADEQLH 240
Db 181 NDYICPATNQCTIDKNRKSCQACRLKCYEYGVNKGSRERCGYLRVRRQSADEQLH 240
Qy 241 CAGKAKSGGCHAPRVRELLLDALSPQQLVTLLEAEPHVLISRPSPAPFTEASMMMSLTK 300
Db 241 CAGKAKSGGHTPLVRELLLDALSPQQLVTLLEAEPHVLISRPSPAPFTEASMMMSLTK 300
Qy 301 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 360
Db 301 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 360
Qy 361 VLDREDEKCVGEILEIFDMLLATTTSRRELKQHKYLCVKA MILLNSMYPLVTATQDA 420
Db 361 VLDREDEKCVGEILEIFDMLLATTTSRRELKQHKYLCVKA MILLNSMYPLVTATQDA 420
Qy 421 DSSRKLHLNVAVDALVWVIAKSGISSQQSRLANLMLLSHVRHSHKNGEHL 477
Db 421 DSSRKLHLNVAVDALVWVIAKSGISSQQSRLANLMLLSHVRHSHKNGEHL 477

RESULT 3
Q95ME9
ID Q95ME9 PRELIMINARY; PRT; 486 AA.
AC Q95ME9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Estrogen receptor beta 2.
GN ERBT2A2.
OS Callithrix jacchus (Common marmoset).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OC NCBI_TaxID=9483;
```



[1]  
RP SEQUENCE FROM N.A.  
RA Scobie G.A., Wilson J.A., Millar M.R., Macpherson S., Saunders P.T.;  
RT "The estrogen receptor beta variant ERbeta2 is expressed in  
a wide range of tissues in both Old and New World primates."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
DR EMBL; AF393816; AAK71318.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR InterPro; IPR000536; F:steroid hormone receptor; IEA.  
DR InterPro; IPR001723; Steroid hormone receptor.  
DR InterPro; IPR008946; Steroid hormone receptor.  
DR InterPro; IPR001628; Zinc finger.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00398; STRDHORMONER.  
DR PRINTS; PR00047; STROIDFINGER.  
DR ProDom; PD000035; Zinc finger.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; Znf C4; 1.  
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
KW Transcription regulation; Zinc; Zinc-finger.  
SQ SEQUENCE 486 AA; 54344 MW; 4B29385B7371F277 CRC64;  
  
Query Match 82.6%; Score 2317; DB 6; Length 486;  
Best Local Similarity 91.0%; Pred. No. 4.9e-204;  
Matches 434; Conservative 18; Mismatches 25; Indels 0; Gaps 0;  
  
Qy 1 MDINKSPSSNSPSSNCSSQILPLEHGSYIIPSSYDSSHHYEPAMTFYSPAWNYSIPS 60  
Db 1 MDINKSPSSNSPSSNFGSILPLEHGPYIIPSSYVSHHYPAMTFYSPAWNYSIPS 60  
  
Qy 61 NVTNLEGGPGKQTTSPNVLTPGHLSPVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 120  
Db 61 SVTNLEGGPGKQITSPNKLASTPGHLSPVAVHQLSHLYAEPQKSPWCEARSLEHTLPVS 120  
  
Qy 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSYASGYHYGVWVSCGCKAFKRSIQGH 180  
Db 121 RETLKRKVSNGHCASPVTPGSKRDAHFCVCSYASGYHYGVWVSCGCKAFKRSIQGH 180  
  
Qy 181 NDYICPATNCTIDKRRKSCQACRLKRCYEVGMVKCGRRRCGYELVRRORSADQLH 240  
Db 181 NDYICPATNCTIDKRRKSCQACRLKRCYEVGMVKCGRRRCGYELVRRORSADQLH 240  
  
Qy 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPPTASNMMSLTK 300  
Db 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPPTASNMMSLTK 300  
  
Qy 301 LADKELVEMISWAKKIPGFVELSLPQVRLLESCHMEVLMWGLMWSIDHFGKLIAPDL 360  
Db 301 LADKELVEMISWAKKIPGFVELSLDQVRLLESCHMEVLMWGLMWSIDHFGKLIAPDL 360  
  
Qy 361 VLDRDEGKCVGILEIFDMLATTSRRELKQHEYLCKVAMILLNSMYPLVATQDA 420  
Db 361 ILDRDEGKCVGILEIFDMLATTSRRELKQHEYLCKVAMILLNSMYPLVATQDA 420  
  
Qy 421 DSSRLKLAHLNAVTDALVWVIAKSGISSQQOSMELANLMLLSHVHRASNKGMHLL 477  
Db 421 ESSQKLAHLNAVTDALVWVIAKSGISSQQOSMELANLMLLSHVHRASNKGMHLL 477

RESULT 4  
Q91286 PRELIMINARY; PRT; 503 AA.  
ID Q91286;  
AC Q91286;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Estrogen receptor beta type II splice variant.  
GN ESR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_TaxID=10090;  
RP SEQUENCE FROM N.A.  
RC STRAIN=DDY;  
RA Dang Z., van Bezooijen R., Karperien M., Papapoulos S., Lowik C.;  
RT "Exposure of K5483 cells to estrogen enhances osteogenesis and  
inhibits adipogenesis."  
RL J. Bone Miner. Res. 0:0-0(2001).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
DR EMBL; AI054413; AAL15175.1; -.  
DR MGD; MGI:109392; ESR2.  
DR GO; GO:0005496; F:steroid binding; IEA.  
DR GO; GO:0007420; P:brain development; IMP.  
DR GO; GO:0006928; P:cell motility; IMP.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000536; Hormone\_rec\_lig.  
DR InterPro; IPR001723; Steroid hormone receptor.  
DR InterPro; IPR008946; Steroid hormone receptor.  
DR InterPro; IPR001628; Zinc finger.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00398; STRDHORMONER.  
DR PRINTS; PR00047; STROIDFINGER.  
DR ProDom; PD000035; Zinc finger.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; Znf C4; 1.  
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
KW Transcription regulation; Zinc; Zinc-finger.  
SQ SEQUENCE 503 AA; 56072 MW; D68538FD3693251 CRC64;

Query Match 81.0%; Score 2273; DB 11; Length 503;  
Best Local Similarity 85.7%; Pred. No. 5.7e-302;  
Matches 431; Conservative 22; Mismatches 30; Indels 18; Gaps 1;  
  
Qy 46 MTFYSPAVWNYSTPSNVNLTGEGPGKQTTSPNVLTPGHLSPVVRHQLSHLYAEPQKS 105  
Db 1 MTFYSPAVWNYSTPSNVNLTGEGPGKQTTSPNVLTPGHLSPVVRHQLSHLYAEPQKS 105  
  
Qy 106 PWCEARSLEHTLPVNRRETLKRKVSNGRCASPVTPGSKRDAHFCVCSYASGYHYGVWS 165  
Db 61 PWCEARSLEHTLPVNRRETLKRKVSNGRCASPVTPGSKRDAHFCVCSYASGYHYGVWS 165  
  
Qy 166 CEGCKAFKRSIQGHNDYICPATNCTIDKRRKSCQACRLKRCYEVGMVKCGRRRCOG 225  
Db 121 CEGCKAFKRSIQGHNDYICPATNCTIDKRRKSCQACRLKRCYEVGMVKCGRRRCOG 225  
  
Qy 226 YRLVRQRSADQLHFCAGKAKSGGHAPRVRELLDALSPEQLVLTLEAEPPHVLISR 285  
Db 181 YRLVRQRSADQLHFCAGKAKSGGHAPRVRELLDALSPEQLVLTLEAEPPHVLISR 285  
  
Qy 286 SAPPTASNMMSLTKLADKELVEMISWAKKIPGFVELSLPQVRLLESCHMEVLMWGLM 345  
Db 241 SAPPTASNMMSLTKLADKELVEMISWAKKIPGFVELSLPQVRLLESCHMEVLMWGLM 345  
  
Qy 346 RSIDHFGKLIAPDLVLD-----RDEGKCVGILEIFDMLATTSR 387  
Db 301 RSIDHFGKLIAPDLVLD-----RDEGKCVGILEIFDMLATTSR 387  
  
Qy 388 RELKQHEYLCKVAMILLNSMYPLVATQDASSRLKLAHLNAVTDALVWVIAKSGIS 447  
Db 361 RELKQHEYLCKVAMILLNSMYPLVATQDASSRLKLAHLNAVTDALVWVIAKSGIS 447  
  
Qy 448 SQOSMELANLMLLSHVHRASNKGMHLLNMCKNVVPPVLDLLEMLNAFVLRGKSSI 507  
Db 421 SQOSMELANLMLLSHVHRASNKGMHLLNMCKNVVPPVLDLLEMLNAFVLRGKSSI 507

DE OS Estrogen receptor beta.  
 OS Squalus acanthias (Spiny dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.  
 OX NCBI\_TaxID=7797;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sikora R., Betka M., Callard G.V.;  
 RT "Molecular Cloning and Stage-Related Expression of an Estrogen  
 RT Receptor Beta Subtype During Spermatogenesis in the Dogfish Shark  
 RT (Squalus Acanthias) Testis";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: AF147746; AAK57823.1; --  
 DR HSP: P15793; 1LBD.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003707; P:steroid hormone receptor activity; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO: GO:0006350; P:transcription; IEA.  
 DR InterPro: IPR000536; Hormone rec lig.  
 DR InterPro: IPR001723; Strdhmrn\_receptor.  
 DR InterPro: IPR008946; Str\_ncl\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00104; hormone rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00398; STRDHORMONER.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid; 1.  
 DR SMART: SM00430; HOLI\_1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 DR PROSITE: PS00031; Nuclear protein; Receptor; Transcription;  
 DR DNA-binding; Metal-binding; Zinc-finger.  
 DR Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 542 AA; 61285 MW; D539A29A9718DD37 CRC64;

Query Match 60.3%; Score 1691; DB 13; Length 542;  
 Best Local Similarity 61.7%; Pred. No. 1.9e-146; Indels 18; Gaps 7;  
 Matches 320; Conservative 83; Mismatches 98;

Qy 3 IKNSPSSLSNPSYNSQSILP--LEHGSIIYPSYVDSHSHYEPAMTFYSPAVNYSIPS 60  
 Db 27 IKNSPGLTTPQYS---STLPGISEHGPVCIPISSYVENRHEFTTAFYSPILGYSMPS 83  
 Qy 61 NVTNLEGGPQRTTSPNVLWPTPGHLSPLVVRQLSHLYABPQSPKCEARSLSLHTLPVN 120  
 Db 84 DASGPDGTIVRQSLSPSMYSSTGHVSPITLHCQQPTMYABPPKSPMDLRLSGDQHL-LN 142  
 Qy 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGWSCEGCKAFFKRSIQGH 180  
 Db 143 RENLKKPAPP--GSSVNGYCSRDHAFCAVCSYASGYHYGWSCEGCKAFFKRSIQGH 200  
 Qy 181 NDYICPATNQCTIDKNRKSQACRLKCYEVMYKGSRRRCGYRLVRRQSADEQLH 240  
 Db 201 NAVICPATNQCTIDKNRKSQACRLKCYEVMYKGSRRRCGYRLVRRQSADEQLH 260  
 Qy 241 CAGKAKESG-GHAPRVRELLDLSPEQLVLTLLAEPPHVL-ISRPSAPFTASMMMSL 298  
 Db 261 HWGRKRSGETNTISDTCLNELAEKLLSSILEAEPPNYSILNHNKPYTEVSQMSL 320  
 Qy 299 TKLADKELVHMSWAKKIPGVFELSIFDQVRLLESQMSVLMGLMWRSDHFGKLIAP 358  
 Db 321 TNLADRELVHMSWAKKIPGVFELDLHDQVQLLECCWLEVLVGLMWRSEIYFGKLIAP 380  
 Qy 359 DLVLDREDEGKVEGILEIFDMLATTSRFRKLQHKVEYLCVKAMILLNSMYPLVTATQ 418  
 Db 381 DLILDRDEGQCVGILEIFDMLAATSRFRKLQHKVEYLCVKAMILLNSMYPLVTATQ 440  
 Qy 419 DADSSRKLAHLNAVTDALVWVIAKSGISSQSQSMRLANILLSHVRRHASKNGMEHLN 478  
 Db 441 EHNRKRLKILDTITDTLWCMKSGIPPOQQAATRLAHLMLLSHLRHSASKNGMEHLYS 500

Qy 508 TGSCESPAEDSKSKEGSGNQPSQ 530  
 Db 481 SGSECCSTEDSKSKEGSGNQLSQ 503

RESULT 5  
 Q86231 PRELIMINARY; PRT; 323 AA.  
 AC Q86231;  
 DT 01-JUN-2003 (Tremblrel. 24, Created)  
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical 35.9 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC024181; AAH24181.1; --  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR008946; Str\_ncl\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid; 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 323 AA; 35944 MW; 158D376C56D3CA12 CRC64;

Query Match 61.4%; Score 1723; DB 4; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-149; Indels 0; Gaps 0;  
 Matches 318; Conservative 0; Mismatches 0;

Qy 1 MDIKNSPSSLSNPSYNSQSILPHEGSIYIPSSYVDSHSHYEPAMTFYSPAVNYSIPS 60  
 Db 1 MDIKNSPSSLSNPSYNSQSILPHEGSIYIPSSYVDSHSHYEPAMTFYSPAVNYSIPS 60  
 Qy 61 NVTNLEGGPQRTTSPNVLWPTPGHLSPLVVRQLSHLYABPQSPKCEARSLSLHTLPVN 120  
 Db 61 NVTNLEGGPQRTTSPNVLWPTPGHLSPLVVRQLSHLYABPQSPKCEARSLSLHTLPVN 120  
 Qy 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGWSCEGCKAFFKRSIQGH 180  
 Db 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGWSCEGCKAFFKRSIQGH 180  
 Qy 181 NDYICPATNQCTIDKNRKSQACRLKCYEVMYKGSRRRCGYRLVRRQSADEQLH 240  
 Db 181 NDYICPATNQCTIDKNRKSQACRLKCYEVMYKGSRRRCGYRLVRRQSADEQLH 240  
 Qy 241 CAGKAKESG-GHAPRVRELLDLSPEQLVLTLLAEPPHVLISRPSAPFTASMMMSLTK 300  
 Db 241 CAGKAKESG-GHAPRVRELLDLSPEQLVLTLLAEPPHVLISRPSAPFTASMMMSLTK 300  
 Qy 301 LADKELVHMSWAKKIPG 318  
 Db 301 LADKELVHMSWAKKIPG 318

RESULT 6  
 Q90ZE6 PRELIMINARY; PRT; 542 AA.  
 AC Q90ZE6;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

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OY 479 MKCKNVVYVDLLEMLNAHVLRGCKSSITGSCSPAED 517
DB 501 MKCKNVVYVDLLEMLDAHVY-----SRTPSD 531

RESULT 7
O8CGK9 PRELIMINARY; PRT; 335 AA.
AC O8CGK9
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Estrogen receptor 2 (fragment).
GN RSR2
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Zhang X., Harris H.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY172105; C:nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Sterhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR SMART; SM00430; HOLI; 1.
DR NON TER
FT NON TER
SQ SEQUENCE 335 AA; 37779 MW; F8B014F3EA7A80 CRC64;

Query Match 55.4%; Score 1553; DB 11; Length 335;
Best Local Similarity 89.3%; Pred. No. 4.6e-134;
Matches 299; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

OY 196 NRRKSCQACRLKCYEYGVWYKCGSRRCGYRLVRRQSRADQLHCAGKAKRGSGHAPRV 255
DB 1 NRRKSCQACRLKCYEYGVWYKCGSRRCGYRVVRRQSRSPGQLHCLSKAKHGHTPRA 60

OY 256 RELLDALSPEQLVLTLEAPPHVLSRPSAPFTASMMSLTKLADKELVHMSKAK 315
DB 61 RELLDALSPEQLVLTLEAPPHVLSRPSAPFTASMMSLTKLADKELVHMSKAK 120

OY 316 IPGFVELSLFDQVRLLESCHMEVLMGLMWSRIDHPGKLIAPDPLVLRDDEGKCVGILE 375
DB 121 IPGFVELSLFDQVRLLESCHMEVLMGLMWSRIDHPGKLIAPDPLVLRDDEGKCVGILE 180

OY 376 IPDMLATTSRFRKLQKHEYLVCVKAMILLNSMYPVLTATQDADSSRKLALHNAVTD 435
DB 181 IPDMLATTSRFRKLQKHEYLVCVKAMILLNSMYPVLTATQDADSSRKLALHNAVTD 240

OY 436 ALVWVIKSGISSQOQSMRLANILMLSHVRHASNKGHEHLNKKCNVVPVYDILLLEML 495
DB 241 ALVWVIKSGISSQOQSMRLANILMLSHVRHASNKGHEHLNKKCNVVPVYDILLLEML 300

OY 496 NAHVLRGCKSSITGSCSPAEDSKSGSQNSQ 530
DB 301 NAHVLRGCKSSITGSCSPAEDSKSGSQNSQ 335

RESULT 8
O8JJB9 PRELIMINARY; PRT; 559 AA.
AC O8JJB9
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DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 25, Last annotation update)
DE Estrogen receptor beta.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Watabe S., Matsumoto T., Kobayashi M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AB083064; BAB91218.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Sterhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger
SQ SEQUENCE 559 AA; 62269 MW; IB5849F5E8117FF3 CRC64;

Query Match 52.5%; Score 1471.5; DB 13; Length 559;
Best Local Similarity 55.4%; Pred. No. 2.9e-126;
Matches 297; Conservative 80; Mismatches 130; Indels 29; Gaps 12;

OY 12 SPSSVNCSSILPLEHGSIYI2SSVVDSSHYPAMTFYSPAVMYISIPSNVNLGGPG- 70
DB 28 SP-ARNSSPSLPVESHPICFSPYDLSHDPTTLPFFYSFALLGY----GAAPLSDCPSV 82

OY 71 ROTTSPNVLPPTPGHLSPLVVRQLSHLYA-BQKSPWCEARSLBHTLPVNRRL-RRKV 128
DB 83 RQSLSPSLFPWPHNVSSVVLHQQTQLQNHPTGSMWELTPHDSBEENCKPLAKRVA 142

OY 129 SGNRCASPVTCGSKRDAHFCAVCSDIYASGHYGVWSCGCKAFPKRSIQGHNDYICPAT 188
DB 143 DAETSASLRG---RADMHYCAVCSDIYASGHYGVWSCGCKAFPKRSIQGHNDYICPAT 199

OY 189 NOCTIDKRRKSCQACRLKCYEYGVWYKCGSRRCGYRLVRRQSRADQ--LHCAGKAK 246
DB 200 NOCTIDKRRKSCQACRLKCYEYGVWYKCGSRRCGYRLVRRQSRADQ--LHCAGKAK 255

OY 247 RSGGHAPRV-----ELLDALSPEQLVLTLEAPPHV-LISRPSAPFTASMM 296
DB 256 TCGPRSQIKSVPRPLGKNKVSIALSPBELIARINDAEPPIYLMNDVKCPTEANIMM 315

OY 297 SLTKLADKELVHMSKAKIPGFVELSLFDQVRLLESCHMEVLMGLMWSRIDHPGKLI 356
DB 316 SLTKLADKELVHMSKAKIPGFVELSLFDQVRLLESCHMEVLMGLMWSRIDHPGKLI 375

OY 357 APDVLDRDDEGKCVGILEIPDMLATTSRFRKLQKHEYLVCVKAMILLNSM-YPLVT 415
DB 376 SPDLSLSRDEGSCVQGFVEIFDMLLAATSRFRKLQKHEYLVCVKAMILLNSMCLSSAE 435

OY 416 ATQDADSSRKLALHNAVTDALVWVIKSGISSQOQSMRLANILMLSHVRHASNKGHEH 475
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Db 436 GGELOQRSKLLCLDSDVTDALWAIKVTGLSFQORSTRLAHLLMLLSHRHNSKGMHDH 495
Qy 476 LANKKCNVWPVYDLEMLNAHVLRCGSKSITGSECSA-EDSKSGEQSNPQSQ 530
Db 496 LHCMMKQKQVPLDYDLEMLDAHIMHSSRLSHSGPRAAPAPKESKGVQEQALTRTSQ 551

RESULT 9
Q7ZU32 PRELIMINARY; PRT; 553 AA.
AC Q7ZU32;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Esr2a protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green S.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044349; RAH44349.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Steroid receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STEROIDHORMONER.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR SEQUENCE 553 AA; 62339 MW; 1E7E78A66AD7A53 CRC64;

Query Match 51.9%; Score 1455.5; DB 13; Length 553;
Best Local Similarity 55.7%; Pred. No. 8.3e-125;
Matches 290; Conservative 78; Mismatches 126; Indels 27; Gaps 9;

Qy 16 YNCSQILPLEHGSIVPSSYVDSHHEPAMTFYSPAVKNSIP--SNVTNLEGGFGQRT 73
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Db 31 FNSSPSLFVNHPIPIPSPYDLDGHDFTLFPYSPALLGYSTPLSDCSSV-----RQS 85
Qy 74 TSNVLWPTFGHLSPLVHHRQLSHLYABPKQSPWCARSLEHTLPVNRRTLLKRVKSGNRC 133
Db 86 LSPTLFWPSPHSHVSLTLQQSRLOQNATSGTWTHTPHDHYVEEENSPLVKRVADTEE 145
Qy 134 ASPTVGPGRDAHFCVAGSDYASGVHYGVMSCEGCAFFKESIQGHNDYICPATNOCTI 193
Db 146 TS--VSLRGKADHVCVSDYASGVHYGVMSCEGCAFFKESIQGHNDYICPATNOCTI 203
Qy 194 DKNRKSCQACRLKCYEYGVMSKRRRCYRLVRORSADQ--LHCAGKAKSGGH 251
Db 204 DKNRKSCQACRLKCYEYGVMSKRRRCYRLVRORSADQ--LHCAGKAKSGGH 259
Qy 252 ARVR-----ELLDALSPQQLAVTLRAEPHV-LISRSPAPFTEASMMSLTKL 301
Db 260 SBIKIPRLSPNEVRLSPLESLIRIMRABPEIYDKMKKPFTEAYANVMSLTNL 319
Qy 302 ADKELVHMISWAKKIPGVFVLSLFDQVRLLESCEWMEVLMGLMWRSIDHPGKLIIPADLV 361
Db 320 ADKELVHMISWAKKIPGVFVLSLFDQVRLLESCEWMEVLMGLMWRSIDHPGKLIIPADLV 379
Qy 362 LDRDEKCVETILEIFDMILLATSRRELKLOHKEYLCVKAMILLNSM-YPLVATATODA 420
Db 380 LSRDESSCVGLVEIFDMILLATSRRELKLOHKEYLCVKAMILLNSM-YPLVATATODA 439
Qy 421 DSRKLAHLINAVTDALWAIKVTGLSFQORSTRLAHLLMLLSHRHNSKGMHDH 480
Db 440 QSRSKLLCLDSDVTDALWAIKVTGLSFQORSTRLAHLLMLLSHRHNSKGMHDH 499
Qy 481 CKNVFVYDLEMLNAHVLRCGSKSITGSECSA-EDSKS 520
Db 500 MKQNVPLDYDLEMLDAHIMHSSRLSHSGPRAAPAHKDKNS 540

RESULT 10
Q90WS8 PRELIMINARY; PRT; 553 AA.
AC Q90WS8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ZFER-beta2 protein.
GN ZFER-BETA2
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1];
RP SEQUENCE FROM N.A.
RA Mennet A., Pellegrini E., Anglade I., Blaise O., Laudet V., Kah O.,
RA Pakdel F.;
RT "Binding characteristics, transactivation properties and central
RT expression of three estrogen receptor subtypes in zebrafish."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AJ414567; CAC93849.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroid receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STEROIDHORMONER.
DR PRINTS; PR00447; STEROIDFINGER.
```

GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 InterPro: IPR000536; Hormone\_rec\_lig.  
 InterPro: IPR001733; Stdhmn\_receptor.  
 InterPro: IPR008946; Str\_nc1\_receptor.  
 InterPro: IPR001628; Znf\_C4steroid.  
 Pfam: PF00104; hormone\_rec; 1.  
 Pfam: PF00105; zf-C4; 1.  
 PRINTS: PR00398; STROHORMONER.  
 PRINTS: PR00047; STROIDPFINGER.  
 ProDom: PD000035; Znf\_C4steroid; 1.  
 SMART: SM00430; HOLI; 1.  
 SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW Receptor.  
 SQ SEQUENCE 553 AA; 62196 MW; 928FC9E0D339844B CRC64;

Query Match 51.4%; Score 1441.5; DB 13; Length 553;  
 Best Local Similarity 55.3%; Pred. NO. 1.6e-123; Indels 27; Gaps 9;  
 Matches 288; Conservative 76; Mismatches 130;

QY 16 YNCSQSILPLEHGSIVIPSSYVDSHHIEYFAMTYFSPAVMNYISIP--SNVTNLEGGPQRQT 73  
 DB 31 FNSSSPSLAVENHPICIIPSPYTDLGHDFSLPFVSPALLGYSTSPISDCSSV-----RQS 85  
 QY 74 TSPNVLWPFEGHLSPLVHRLSHLVAEPKQSPWCARSLEHLTPVNRFLTKKVKSGNRC 133  
 DB 86 LSPTLEFPWPHSHVSSLTLOQSSRLQONHATSGTWTEHPDHVEEENSKFLVKPVAETEE 145  
 QY 134 ASPVTGPGSRDAHFAVCSDYASGTHYGVNSCEGCKAFKRSIQGHNDYICPATNCTI 193  
 DB 146 TS--VSLRGKADWHYCAVCSYASGTHYGVNSCEGCKAFKRSIQGHNDYICPATNCTI 203  
 QY 194 DKNRRKSCQACRLRKCYEVMGVCGRRRRCGYLVRQRSAD EQ--LHCAGKAKRSGGH 251  
 DB 204 DKNRRKSCQACRLRKCYEVMGVCGRRRRSSY---QQRGAQKRLVRFSGRVMRTGPR 259  
 QY 252 APVREL-----LLDALSPQQLVLTLEARPVH-LISPSAPPTASMMMSLTKL 301  
 DB 260 SQBIKSIPLRPLSGNEGARISLSPLEELSRITWEABPEIYLMKMKKFTTEANVMKSLTNL 319  
 QY 302 ADKELVHMSIWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDIHFGKLIIFAPDLV 361  
 DB 320 ADKELVHMSIWAKKIPGFVLSLFDQVHLLCCWLEVLMLGLMWRSVNHRKLIIFSPDL 379  
 QY 362 LDRDEKCVGILEIFDMLIATTSRRRELKLOHKEYLCVKAMILLNSSM-YPLVTATQDA 420  
 DB 380 LSRDESSCQGLVEIFDMLAASTRRELKQREYVCLKAMILLNSSMCLGSGSEGEDL 439  
 QY 421 DSRKRLAHLNATVDALVWVIAKSGISSQQSSQSRNLANLLMLSHVRHASNKGMEHLNKK 480  
 DB 440 QSRKLLCLLDSYTDALVWAIKTLGSFQQRSTRLAHLMLSHIRHVSNGKMDHLCKMK 499  
 QY 481 KKNVVPYDILLMLNHLVLRGCKSSITGSCSPFA-EDSKS 520  
 DB 500 MKKNVAPLYDILLMLDAHMHSSRLSHSGPRAPAHHKDNKS 540

RESULT 12  
 Q8QHK9  
 ID Q8QHK9 PRELIMINARY; PRT; 565 AA.  
 AC Q8QHK9  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Estrogen receptor beta.  
 GN ERB.  
 OS Paralichthys olivaceus (Flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectoidei; Paralichthyidae; Paralichthys.  
 OC NCBI\_TaxID=8255;  
 RN [1]



QY 178 QGHNDYICPATNQCTIDKNNRKSQACRLKCYEYGVKQSGRRRCGRLVRRORSAD 237  
Db 185 QGHNDYICPATNQCTIDKNNRKSQACRLKCYEYGVKQSGRRRCGRLVRRORSAD 242  
QY 238 QHCHGAKRSGHAPRVRELL---DALSPQLVLTLEAPPHV-LISPSAPPTAS 293  
Db 243 RLSSQGT-----NGEAVGLAPOPPALTSKQLIERIEAPPEIYLMKQVRRPLTEAN 297  
QY 294 NMMSLTKLADKELVHMISWAKKIPGVFVLSLFDQVRLLESCHMEVLMGLMWSRSDHPGK 353  
Db 298 IMMSLTNLADKELVHMISWAKKIPGVFVLSLFDQVRLLESCHMEVLMGLMWSRSDHPGK 357  
QY 354 LIPAPDLVDRDEGKCVGILIFDMLATTFRFRELKLOHKEYLVCVQAMILLNSM-YP 412  
Db 358 LIFSPDLSLRBEGSCVOGFLBIFDMLIAATSRVRELKLOHKEYLVCVQAMILLNSMCLS 417  
QY 413 LVTATODADSSKLAHLNAVTDALVWIAKSGISSQOOSMELANMLLSHVRHASNKG 472  
Db 418 SEGSELSQSKLLELDVAVTALVWIAKSGISSQOOSMELANMLLSHVRHASNKG 477  
QY 473 MEHLNLMKCNVVPVYDVLLEMLNAHVL-----RGCKSSITGSECSPAEDSKSKEGSON 526  
Db 478 MDHLGKMKCNVVPVYDVLLEMLNAHVL-----RGCKSSITGSECSPAEDSKSKEGSON 533  
QY 527 P 527  
Db 534 P 534  
RESULT 14  
Q7T2K7 PRELIMINARY; PRT; 671 AA.  
AC Q7T2K7  
DT 01-OCT-2003 (TREMELrel. 25, Created)  
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Estrogen receptor beta.  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;  
OC Labridae; Halichoeres.  
OX NCBI\_TaxID=217853;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Park J.-G., Kim S.-J.;  
RT "Molecular cloning and expression of two estrogen receptor subtypes in  
protogynous wrasse, Halichoeres tenuispinis."  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AV305027; AAP72179.1;  
KW Receptor.  
SQ SEQUENCE 671 AA; 74781 MW; 5373F8129DF71C6A CRC64;  
Query Match 49.9%; Score 1401; DB 13; Length 671;  
Best Local Similarity 52.4%; Pred. No. 1.le-119;  
Matches 300; Conservative 73; Mismatches 127; Indels 72; Gaps 17;  
QY 5 NSPSSINSPSYNCQSILPLEHSGSYIPSSVYDSHVEY-----PAMTFYSPAMVNYSPS 60  
Db 30 SSPGLL--PAVYSPRQ--WDSHVTIPSPYDNNQYHNGSGSVSFSPSVLVARPS 84  
QY 61 NVTNLEG--QPGRQITSPNVLTPTGSLSPVVRQL-----SHLYAEFPQKSPWC 108  
Db 85 ATDPSPLSGP---LSPSAFWPP--HSQPNLPSLTLCRCPQPLGVNESGLHA-----PWL 133  
QY 109 EAR-----SLEHTLPVNRETLKKVSG-----NRCASPVTPGSKVEDAFCHVCSQDYS 157  
Db 134 ESKPHNISSSSSIGCNKPKLGKSEBGNVGNPFLSSSVV-----GRADMEHFCVACHDYS 189  
QY 158 GYHYGVWSCGCKAFFKRSIQGHNDYICPATNQCTIDKNNRKSQACRLKCYEYGVKQSG 217  
Db 190 GYHYGVWSCGCKAFFKRSIQGHNDYICPATNQCTIDKNNRKSQACRLKCYEYGVKQSG 249

QY 218 GSRRECGYRLVRRORS-----ADBQLHCAGKAKSGGH-----APRVREL 258  
Db 250 GVRERCSTGTRHRRGGLQPRDPTGRGLVRVGLSGRAQRHLHLEGPLTPTVPLPQMSHV 309  
QY 259 LLDALSPQLVLTLEAPPHV-LISPSAPPTASNMMSLTKLADKELVHMISWAKKIP 317  
Db 310 HHAAMSPEEFIMRIEAEPEIYLMEEQKQPFTEASNMMSLTNLADKELVHMISWAKKIP 369  
QY 318 GFVLSLFDQVRLLESCHMEVLMGLMWSRSDHPGKLIFFAPDLVDRDEGKCVGILIF 377  
Db 370 GFVELCLADQHLHLLKCCWLBILMLGLMWSRSDHPGKLIFSPDFKLNREEGQCVGIMEIF 429  
QY 378 DMLATTFRFRELKLOHKEYLVCVQAMILLNSMYPVLTAT-ODADSSKLAHLNAVTD 436  
Db 430 DMLAAATSRFRELKLOHKEYLVCVQAMILLNSMYPVLTAT-ODADSSKLAHLNAVTD 489  
QY 437 LVWIAKSGISSQOOSMELANMLLSHVRHASNKGMEHLNLMKCNVVPVYDVLLEMLN 496  
Db 490 LVWIAKSGISSQOOSMELANMLLSHVRHASNKGMEHLNLMKCNVVPVYDVLLEMLN 549  
QY 497 AHVLRGCKSSITGSECSPAEDSKSKEGSONPQ 528  
Db 550 ANT---SSSGSSQSSSPNSDSYS-DLHQYPO 577  
RESULT 15  
Q9OWS9 PRELIMINARY; PRT; 592 AA.  
AC Q9OWS9  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE ZFER-beta1 protein.  
GN ZFER-BETA1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Menuet A., Pellegri E., Anglade I., Blaise O., Laudet V., Kah O.,  
RC Pakdel F.;  
RT "Binding characteristics, transactivation properties and central  
expression of three estrogen receptor subtypes in zebrafish."  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
DR EMBL: AJ414566; CAC3848.1;  
DR HSSP: P19793; ILBD.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0005489; P:electron transporter activity; IEA.  
DR GO: GO:0003707; P:steroid hormone receptor activity; IEA.  
DR GO: GO:0003700; P:transcription factor activity; IEA.  
DR GO: GO:0006118; P:regulation of transcription; IEA.  
DR GO: GO:0006350; P:transcription; IEA.  
DR InterPro: IPR000345; CytC\_heme\_BS.  
DR InterPro: IPR000336; Hormone\_rec\_lig.  
DR InterPro: IPR001723; Ster\_hrmn\_rec.  
DR InterPro: IPR008946; Str\_ncl\_receptor.  
DR InterPro: IPR001628; Znf\_C4steroid.  
DR Pfam: PF00104; hormone\_rec; 1.  
DR Pfam: PF00105; zf-C4; 1.  
DR PRINTS: PR00398; STRDHORMONER.  
DR PRINTS: PR000035; Znf\_C4steroid; 1.  
DR SMART: SM00430; HOLI\_1.  
DR SMART: SM00399; ZNF\_C4; 1.  
DR PROSITE: PS00190; CYTOCHROME\_C; 1.  
DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

KW Transcription regulation: Zinc; Zinc-finger.  
SQ SEQUENCE 592 AA; 66046 MW; 7F65218E2C03F1B8 CRC64;

Query Match 49.8%; Score 1397.5; DB 13; Length 592;  
Best Local Similarity 51.6%; Pred. No. 1.9e-119;  
Matches 300; Conservative 79; Mismatches 121; Indels 81; Gaps 16;

QY 11 NSPSSYNCOSILP-----LEHGSYIPSSVYDSHSEYP-----AMTFYSP- 51  
DB 13 SSKADRGASPALPLPLASPLGMDNQTCIPSPYACADYSPHGGEFNGHGLTLYSPV 72

QY 52 --AVNYSIPNVNLEGGGRQTTSPNVLPTGHL---SPLVVRQLSHLYABPOKSP 106  
DB 73 SSAVLGFRPPVSESL-----VPLSPTILWP-PHSLHCPPLAYSETRSH-----SA 118

QY 107 WCEARSLEHTLPVNRKTLK-----RKVSGNRKASPTVPGSKRDADHFCVCSYASGYH 160  
DB 119 WEERAT--HTLSQSSVLSHTKLQQLEGNGLNPASIVGKGDTHTFCAVCHDYASGYH 176

QY 161 YGVNSCEGCKAFFKRSIQHNDYICPATNQCTIDNRRKSCQACRLRKCVEVGMVKCGR 220  
DB 177 YGVNSCEGCKAFFKRSIQHNDYICPATNQCTIDNRRKSCQACRLRKCVEVGMVKCGR 236

QY 221 RERCYRLVRQR-----SADEQLHCAGKAKR-----SGGHAPRVRELL 260  
DB 237 RERCYRGARHRNPQIRDSSGGVVLGRGQSOHLFPPLSPSOHLFPSSGGRH-EGRAL-- 293

QY 261 DALSPQLVLTLEAPPHVLISRP-SAPFTASMMMSLTKLADKELVHMISWAKKIPGF 319  
DB 294 -NYSPEQLVSCILEAPPOIVIREPVKPYTEASMMMSLTSLADKELVHMISWAKKIPGF 352

QY 320 VELSLFDQVRILLESQWMEVLMGLMWSRIDHFGKLIAPDLVLDRDGKCEGILEIFDM 379  
DB 353 VELTSLDQVHLLECWLIDILMGLMWSVDHPGKLIPTPDKLAREGNCVEGIMBIFDM 412

QY 380 LLATTSRRELKQHKYLCVKAMILLNSMYPLVTAT-QDADSSRKLALHINAVTDALV 438  
DB 413 LLATTSRRELKQREYVCLKAMILLNSNCSLPQTPEDVESRGKVLNLDSDVTDALV 472

QY 439 WVIKSGISSQOOSRNLANLLMLLSHVHSHASNGKMEHLNNKCKNVVPVYDILLEMNAH 498  
DB 473 WIISTRGLSSQOOSIRLAHLMLLSHIRHLNKGIEHLSNKKRNKRVLLYDILLEMNDAN 532

QY 499 VLRGCK-----SSITGSECSPAEDSKSGSQNPQSQ 530  
DB 533 ASQSRMLEDRQOSPENLHTRPQPDLDKDSQETPHSPRAE 573

Search completed: June 20, 2004, 10:38:38  
Job time : 48 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:36:03 ; Search time 23 Seconds  
 (without alignments)  
 1189.642 Million cell updates/sec

Title: US-08-906-365-2  
 Perfect score: 2805  
 Sequence: 1 MDIKNSPSSLNSSSYNCQS.....ECSPABDSKSKESQNPQSQ 530

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued Patents AA:\*  
 1: /cgm2\_6/ptodata/2/iaa/5A COMB.pdp.\*  
 2: /cgm2\_6/ptodata/2/iaa/5B COMB.pdp.\*  
 3: /cgm2\_6/ptodata/2/iaa/6A COMB.pdp.\*  
 4: /cgm2\_6/ptodata/2/iaa/6B COMB.pdp.\*  
 5: /cgm2\_6/ptodata/2/iaa/PTCUS COMB.pdp.\*  
 6: /cgm2\_6/ptodata/2/iaa/backfiles.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	100.0	530	4	US-09-608-088-25
2	2805	100.0	548	3	US-09-139-617-1
3	2805	100.0	548	4	US-09-561-741A-1
4	2805	100.0	548	4	US-09-558-795-1
5	2554	91.1	485	2	US-08-836-620A-3
6	2522	89.9	477	4	US-09-608-088-5
7	2291	81.7	485	2	US-08-836-620A-2
8	2286	81.5	484	2	US-08-836-620A-13
9	2267	80.8	485	2	US-08-836-620A-5
10	2262	80.6	484	2	US-08-836-620A-14
11	2198	78.4	416	4	US-09-608-088-6
12	2198	78.4	418	4	US-09-608-088-21
13	2017	71.9	384	2	US-08-836-620A-15
14	1233.5	44.0	595	3	US-08-764-870-12
15	1233.5	44.0	595	3	US-08-980-115-12
16	1224.5	43.7	595	3	US-09-041-896-35
17	1224.5	43.7	595	4	US-08-453-998-2
18	1222.5	43.6	591	2	US-08-836-620A-17
19	1214.5	43.3	596	2	US-08-836-620A-16
20	1181	42.1	233	4	US-09-608-088-4
21	1160	41.4	410	6	5223606
22	1136.5	40.2	229	3	US-09-249-645-1
23	1111.5	39.6	229	4	US-09-844-132B-1
24	1064	37.9	228	3	US-09-249-645-2
25	1064	37.9	228	4	US-09-844-132B-2
26	1055	37.6	226	2	US-08-836-620A-7
27	810	28.9	773	3	US-08-564-264-1

## ALIGNMENTS

### RESULT 1

US-09-608-088-25  
 ; Sequence 25, Application US/09608088  
 ; Patent No. 6580368  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mosselman, Sietse  
 ; APPLICANT: Dijkema, Rein  
 ; TITLE OF INVENTION: No. 6680368el Estrogen Receptor  
 ; FILE REFERENCE: O/96193 US/D1  
 ; CURRENT APPLICATION NUMBER: US/09/608,088  
 ; CURRENT FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 08/826,361  
 ; PRIOR FILING DATE: 1997-03-26  
 ; PRIOR APPLICATION NUMBER: EP 96203284.3  
 ; PRIOR FILING DATE: 1996-11-22  
 ; PRIOR APPLICATION NUMBER: EP 96200820.7  
 ; PRIOR FILING DATE: 1996-03-26  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 25  
 ; LENGTH: 530  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-608-088-25

Query Match	100.0%;	Score	2805;	DB	4;	Length	530;		
Best Local Similarity	100.0%;	Pred. No.	1.4e-291;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	530;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MDIKNSPSSLNSSPSSYNCSQSLPLEHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNTSIPS	60						
Db	1	MDIKNSPSSLNSSPSSYNCSQSLPLEHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNTSIPS	60						
Qy	61	NVTNLEGGGROTTSPNVLPPTPGHLSPLVHQRQLSHLYAEPKSPWCSEARSLEHTLPVN	120						
Db	61	NVTNLEGGGROTTSPNVLPPTPGHLSPLVHQRQLSHLYAEPKSPWCSEARSLEHTLPVN	120						
Qy	121	RETLKRVKSGNRCASPVTPGSGKRDHAFCAVCSDYASGHHYGVMSCEGCKAFKRSIQGH	180						
Db	121	RETLKRVKSGNRCASPVTPGSGKRDHAFCAVCSDYASGHHYGVMSCEGCKAFKRSIQGH	180						
Qy	181	NDYICPATNQCTIDKRRKSCQACRLKCVEYGVNVCGRRRRCGVLVRRQBSADEQLH	240						
Db	181	NDYICPATNQCTIDKRRKSCQACRLKCVEYGVNVCGRRRRCGVLVRRQBSADEQLH	240						
Qy	241	CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAEPHPHLVLSRPSAPFTTASMMMSLTk	300						
Db	241	CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAEPHPHLVLSRPSAPFTTASMMMSLTk	300						
Qy	301	LADKELVHMI SWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWTRSIDHPGKLI FAPDL	360						

Db 301 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 360  
Qy 361 VLDRDEGKCVBGILEIFDMLLATTSRFRKLQKHEYLCKVAMILLNSMPLVTATODA 420  
Db 361 VLDRDEGKCVBGILEIFDMLLATTSRFRKLQKHEYLCKVAMILLNSMPLVTATODA 420  
Qy 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASKNGMEHLNKK 480  
Db 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASKNGMEHLNKK 480  
Qy 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530  
Db 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 2  
US-09-139-617-1  
; Sequence 1, Application US/09139617  
; Patent No. 6222015  
; GENERAL INFORMATION:  
; APPLICANT: WILKINSON, HILARY  
; TITLE OF INVENTION: ESTROGEN RECEPTOR  
; FILE REFERENCE: 20047Y  
; CURRENT APPLICATION NUMBER: US/09/139,617  
; EARLIER FILING DATE: 1998-08-25  
; EARLIER APPLICATION NUMBER: 60/058,271  
; EARLIER FILING DATE: 1997-09-08  
; EARLIER APPLICATION NUMBER: 60/060,520  
; EARLIER FILING DATE: 1997-09-30  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 548  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-139-617-1

Query Match 100.0%; Score 2805; DB 3; Length 548;  
Best Local Similarity 100.0%; Pred. No. 1.5e-291;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLSNPSSWNCOSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVMNYISIPS 60  
Db 19 MDIKNSPSSLSNPSSWNCOSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVMNYISIPS 78  
Qy 61 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 120  
Db 79 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 138  
Qy 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDDYASGHHYGVWSCGCKAFFKRSIQGH 180  
Db 139 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDDYASGHHYGVWSCGCKAFFKRSIQGH 198  
Qy 181 NDYICPATNOCTIDKRRKSCQACRLKCYEYGVWVKGSRRCRCGYRLVRRQSADEQLH 240  
Db 199 NDYICPATNOCTIDKRRKSCQACRLKCYEYGVWVKGSRRCRCGYRLVRRQSADEQLH 258  
Qy 241 CAGKAKRSGCHAPRVRELLLDALSPEQLVTLLEAPPHVLIISRPSPAPPTASMMSLTK 300  
Db 259 CAGKAKRSGCHAPRVRELLLDALSPEQLVTLLEAPPHVLIISRPSPAPPTASMMSLTK 318  
Qy 301 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 360  
Db 319 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 378  
Qy 361 VLDRDEGKCVBGILEIFDMLLATTSRFRKLQKHEYLCKVAMILLNSMPLVTATODA 420  
Db 379 VLDRDEGKCVBGILEIFDMLLATTSRFRKLQKHEYLCKVAMILLNSMPLVTATODA 438  
Qy 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASKNGMEHLNKK 480  
Db 439 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASKNGMEHLNKK 498

Qy 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530  
Db 499 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 548  
RESULT 3  
US-09-561-741A-1  
; Sequence 1, Application US/09561741A  
; Patent No. 6458551  
; GENERAL INFORMATION:  
; APPLICANT: WILKINSON, HILARY  
; TITLE OF INVENTION: ESTROGEN RECEPTOR  
; FILE REFERENCE: 20047Y  
; CURRENT APPLICATION NUMBER: US/09/561,741A  
; CURRENT FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 09/139,617  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: 60/058,271  
; PRIOR FILING DATE: 1997-09-08  
; PRIOR APPLICATION NUMBER: 60/060,520  
; PRIOR FILING DATE: 1997-09-30  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 548  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-561-741A-1

Query Match 100.0%; Score 2805; DB 4; Length 548;  
Best Local Similarity 100.0%; Pred. No. 1.5e-291;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLSNPSSWNCOSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVMNYISIPS 60  
Db 19 MDIKNSPSSLSNPSSWNCOSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVMNYISIPS 78  
Qy 61 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 120  
Db 79 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 138  
Qy 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDDYASGHHYGVWSCGCKAFFKRSIQGH 180  
Db 139 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDDYASGHHYGVWSCGCKAFFKRSIQGH 198  
Qy 181 NDYICPATNOCTIDKRRKSCQACRLKCYEYGVWVKGSRRCRCGYRLVRRQSADEQLH 240  
Db 199 NDYICPATNOCTIDKRRKSCQACRLKCYEYGVWVKGSRRCRCGYRLVRRQSADEQLH 258  
Qy 241 CAGKAKRSGCHAPRVRELLLDALSPEQLVTLLEAPPHVLIISRPSPAPPTASMMSLTK 300  
Db 259 CAGKAKRSGCHAPRVRELLLDALSPEQLVTLLEAPPHVLIISRPSPAPPTASMMSLTK 318  
Qy 301 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 360  
Db 319 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 378  
Qy 361 VLDRDEGKCVBGILEIFDMLLATTSRFRKLQKHEYLCKVAMILLNSMPLVTATODA 420  
Db 379 VLDRDEGKCVBGILEIFDMLLATTSRFRKLQKHEYLCKVAMILLNSMPLVTATODA 438  
Qy 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASKNGMEHLNKK 480  
Db 439 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASKNGMEHLNKK 498  
Qy 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530  
Db 499 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 548

RESULT 4  
US-09-558-795-1

Sequence 1, Application US/09558795  
Patent No. 6562592  
GENERAL INFORMATION:  
APPLICANT: WILKINSON, HILARY  
TITLE OF INVENTION: ESTROGEN RECEPTOR  
FILE REFERENCE: 20047Y  
CURRENT APPLICATION NUMBER: US/09/558,795  
CURRENT FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 09/139,617  
PRIOR FILING DATE: 1998-08-25  
PRIOR APPLICATION NUMBER: 60/058,271  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: 60/060,520  
PRIOR FILING DATE: 1997-09-30  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 548  
TYPE: PRT  
ORGANISM: HUMAN  
US-09-558-795-1

Query Match 100.0%; Score 2805; DB 4; Length 548;  
Best Local Similarity 100.0%; Pred. No. 1.5e-291;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVVDSSHYPANTFYSPAVMNTSIPS 60  
DB 19 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVVDSSHYPANTFYSPAVMNTSIPS 78  
QY 61 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPKSPWCEARSLEHTLPVN 120  
DB 79 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPKSPWCEARSLEHTLPVN 138  
QY 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHGVMSCEGCKAPFKRSIQGH 180  
DB 139 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHGVMSCEGCKAPFKRSIQGH 198  
QY 181 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKCGSRRCGYRLVRRQRSADQLH 240  
DB 199 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKCGSRRCGYRLVRRQRSADQLH 258  
QY 241 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 300  
DB 259 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 318  
QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLIAPDL 360  
DB 319 LADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLIAPDL 378  
QY 361 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 420  
DB 379 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 438  
QY 421 DSSKLAHLNNAVTDALVWVIAKSGISSQQSQKRLANMLLSHVHASNKGMEHLNNK 480  
DB 439 DSSKLAHLNNAVTDALVWVIAKSGISSQQSQKRLANMLLSHVHASNKGMEHLNNK 498  
QY 481 CKXVVPYDILLEMLNAHVLRGCKSSITGSECSPADSKSKEGSONPQSQ 530  
DB 499 CKXVVPYDILLEMLNAHVLRGCKSSITGSECSPADSKSKEGSONPQSQ 548

RESULT 5  
US-08-836-620A-3  
Sequence 3, Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT: Orphan receptor  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-836-620A-3

Query Match 91.1%; Score 2554; DB 2; Length 485;  
Best Local Similarity 99.8%; Pred. No. 9.7e-265;  
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 MTFYSPAVMNTSIPSNTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPKSPQ 105  
DB 1 MTFYSPAVMNTSIPSNTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPKSPQ 60  
QY 105 PWCEARSLHTLPVNRRETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHGVMS 165  
DB 61 PWCEARSLHTLPVNRRETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHGVMS 120  
QY 166 CEGCKAPFKRSIQGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKCGSRRCG 225  
DB 121 CEGCKAPFKRSIQGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKCGSRRCG 180  
QY 226 YELVRRQRSADQLHCAKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRP 285  
DB 181 YELVRRQRSADQLHCAKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRP 240  
QY 286 SAPFTEASMMWLSLKADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLM 345  
DB 241 SAPFTEASMMWLSLKADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLM 300  
QY 346 RSIDHPGKLIAPDLVLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMIL 405  
DB 301 RSIDHPGKLIAPDLVLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMIL 360  
QY 406 LNSSMYPVTATQDADSSKLAHLNNAVTDALVWVIAKSGISSQQSQKRLANMLLSHV 465  
DB 361 LNSSMYPVTATQDADSSKLAHLNNAVTDALVWVIAKSGISSQQSQKRLANMLLSHV 420  
QY 466 RHASNKGMEHLNNKCKXVVPYDILLEMLNAHVLRGCKSSITGSECSPADSKSKEGSO 525  
DB 421 RHASNKGMEHLNNKCKXVVPYDILLEMLNAHVLRGCKSSITGSECSPADSKSKEGSO 480

RESULT 6  
US-09-608-088-5  
Sequence 5, Application US/09608088

Sequence 1, Application US/09558795  
Patent No. 6562592  
GENERAL INFORMATION:  
APPLICANT: WILKINSON, HILARY  
TITLE OF INVENTION: ESTROGEN RECEPTOR  
FILE REFERENCE: 20047Y  
CURRENT APPLICATION NUMBER: US/09/558,795  
CURRENT FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 09/139,617  
PRIOR FILING DATE: 1998-08-25  
PRIOR APPLICATION NUMBER: 60/058,271  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: 60/060,520  
PRIOR FILING DATE: 1997-09-30  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 548  
TYPE: PRT  
ORGANISM: HUMAN  
US-09-558-795-1

Query Match 100.0%; Score 2805; DB 4; Length 548;  
Best Local Similarity 100.0%; Pred. No. 1.5e-291;  
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVVDSSHYPANTFYSPAVMNTSIPS 60  
DB 19 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVVDSSHYPANTFYSPAVMNTSIPS 78  
QY 61 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPKSPWCEARSLEHTLPVN 120  
DB 79 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPKSPWCEARSLEHTLPVN 138  
QY 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHGVMSCEGCKAPFKRSIQGH 180  
DB 139 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHGVMSCEGCKAPFKRSIQGH 198  
QY 181 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKCGSRRCGYRLVRRQRSADQLH 240  
DB 199 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKCGSRRCGYRLVRRQRSADQLH 258  
QY 241 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 300  
DB 259 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 318  
QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLIAPDL 360  
DB 319 LADKELVHMSWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLIAPDL 378  
QY 361 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 420  
DB 379 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 438  
QY 421 DSSKLAHLNNAVTDALVWVIAKSGISSQQSQKRLANMLLSHVHASNKGMEHLNNK 480  
DB 439 DSSKLAHLNNAVTDALVWVIAKSGISSQQSQKRLANMLLSHVHASNKGMEHLNNK 498  
QY 481 CKXVVPYDILLEMLNAHVLRGCKSSITGSECSPADSKSKEGSONPQSQ 530  
DB 499 CKXVVPYDILLEMLNAHVLRGCKSSITGSECSPADSKSKEGSONPQSQ 548

RESULT 5  
US-08-836-620A-3  
Sequence 3, Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT: Orphan receptor  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

Patent No. 6680368  
GENERAL INFORMATION:  
APPLICANT: Mosselman, Sietse  
APPLICANT: Dijkema, Rein  
TITLE OF INVENTION: No. 6680368 Estrogen Receptor  
FILE REFERENCE: O/96193 US/BI  
CURRENT APPLICATION NUMBER: US/09/608,088  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 08/826,361  
PRIOR FILING DATE: 1997-03-26  
PRIOR APPLICATION NUMBER: EP 96203284.3  
PRIOR FILING DATE: 1996-11-22  
PRIOR APPLICATION NUMBER: EP 96200820.7  
PRIOR FILING DATE: 1996-03-26  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 5  
LENGTH: 477  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-608-088-5

Query Match 89.9%; Score 2522; DB 4; Length 477;  
Best Local Similarity 100.0%; Pred. No. 2.5e-261;  
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

54 MNYISPNVTNLEGGGROTTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPKCRARSL 113  
Db 1 MNYISPNVTNLEGGGROTTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPKCRARSL 60

114 EHTLPVNRETLKRKXVGNRCASPTVPGSKRDAHFCAVCSYASGYHYGWSCEGCKAFF 173  
Db 61 EHTLPVNRETLKRKXVGNRCASPTVPGSKRDAHFCAVCSYASGYHYGWSCEGCKAFF 120

174 KRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGMVKGSRERCGYLVRRQR 233  
Db 121 KRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGMVKGSRERCGYLVRRQR 180

234 SADSOLHCAGKAKSGHAPVRELLDALSPEOLVLTLEAEPPHVLISRPAPPTAS 293  
Db 181 SADSOLHCAGKAKSGHAPVRELLDALSPEOLVLTLEAEPPHVLISRPAPPTAS 240

294 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLWNRSIDHPGK 353  
Db 241 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLWNRSIDHPGK 300

354 LIPADVLDRDEGKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPL 413  
Db 301 LIPADVLDRDEGKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPL 360

414 VTATQDADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHVRHASKGM 473  
Db 361 VTATQDADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHVRHASKGM 420

474 EHLNMRCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSONFQSQ 530  
Db 421 EHLNMRCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSONFQSQ 477

RESULT 7  
US-08-836-620A-2  
Sequence 2, Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORGANISM: Rattus rattus  
US-08-836-620A-2

Query Match 81.7%; Score 2291; DB 2; Length 485;  
Best Local Similarity 88.7%; Pred. No. 1.5e-236;  
Matches 430; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

46 MTFYSPAVMYIPSNVTNLEGGPGROTTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 105  
Db 1 MTFYSPAVMYIPSNVTNLEGGPGROTTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 60

106 PWCEARSLSEHTLPVNRETLKRKXVGNRCASPTVPGSKRDAHFCAVCSYASGYHYGWS 165  
Db 61 PWCEARSLSEHTLPVNRETLKRKXVGNRCASPTVPGSKRDAHFCAVCSYASGYHYGWS 120

166 CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGMVKGSRERCG 225  
Db 121 CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGMVKGSRERCG 180

226 YRLVRRORSADQLHCAGKAKSGHAPVRELLDALSPEOLVLTLEAEPPHVLISRP 285  
Db 181 YRLVRRORSADQLHCAGKAKSGHAPVRELLDALSPEOLVLTLEAEPPHVLISRP 240

286 SAPFTASMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLW 345  
Db 241 SAPFTASMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLW 300

346 RSDHDPGLIFAPDLVLDREKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMIL 405  
Db 301 RSDHDPGLIFAPDLVLDREKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMIL 360

406 LNSSMYPLVATQDADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHV 465  
Db 361 LNSSMYPLVATQDADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHV 420

466 RHASNKGMEHLLNMRCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEG 525  
Db 421 RHASNKGMEHLLNMRCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEG 480

526 NPOSQ 530  
481 NLQSQ 485

RESULT 8  
US-08-836-620A-13  
Sequence 13, Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Orphan receptor

Query Match	Best Local Similarity	Score	DB 2;	Length	484;
Matches 429;	Conservative 23;	Mismatches 32;	Indels 0;	Gaps 0;	
46	MTFYSFVAVNYISPNVNTLEGGGPGRTTSNVLWPTPGHLSPLVVRHQLSHLYAEQKS	105			
1	MTFYSFVAVNYISPNVNTLEGGGPGRTTSNVLWPTPGHLSPLVVRHQLSHLYAEQKS	60			
106	PWCEARSLEHTLPVNRRTKRVGNRCASPTVGTGSRDHAFCVACSDYASGHHYGVWS	165			
61	PWCEARSLEHTLPVNRRTKRVGNRCASPTVGTGSRDHAFCVACSDYASGHHYGVWS	120			
166	CEGCKAFFKRSIQGHNDYICPATNOCTIDKNNRKSQCACRLKCYEVMKCGSRRRCG	225			
121	CEGCKAFFKRSIQGHNDYICPATNOCTIDKNNRKSQCACRLKCYEVMKCGSRRRCG	180			
226	YRLVRRQSRADQOLHAGKAGSGHAPVRRELLDALSPQLVLTLEAPPVHLISRP	285			
181	YRLVRRQSRADQOLHAGKAGSGHAPVRRELLDALSPQLVLTLEAPPVHLISRP	240			
286	SAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLDQVRLLESCKWVLMGLMW	345			
241	SAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLDQVRLLESCKWVLMGLMW	300			
346	RSIDHPGKLIAPDVLDRDEGKCVGEILISFDMLLATTSPRELKLOHKEYLVCVKAMIL	405			
301	RSIDHPGKLIAPDVLDRDEGKCVGEILISFDMLLATTSPRELKLOHKEYLVCVKAMIL	360			
406	LNSSMYPLVATODADSSRLAHNLNAVTDALVWVIAKSGISSQQSQRNLANMLLSHV	465			
361	LNSSMYPLVATODADSSRLAHNLNAVTDALVWVIAKSGISSQQSQRNLANMLLSHV	420			
466	RHASNKGHEHLNMMCKNVVPPVYDILLEMLNAHVLRGCKSSITSGECPADSCKSGSQ	525			
421	RHASNKGHEHLNMMCKNVVPPVYDILLEMLNAHVLRGCKSSITSGECPADSCKSGSQ	480			
526	NPOS 529				
481	NLOS 484				

Db 421 RHISNKGHEHLLSNKCKNNVYVYDILLEMLNAHTLRYKSSISGSGCCSTEDSKSKESQ 480

Qy 526 NPOSQ 530

Db 481 NLQSQ 485

RESULT 10

US-08-836-620A-14

; Sequence 14, Application US/08836620A

; Patent No. 5958710

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Orphan receptor

; NUMBER OF SEQUENCES: 19

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,620A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP96/03933

; FILING DATE:

; APPLICATION NUMBER: GB 9518272.1

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9605550.4

; FILING DATE: 15-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9607532.0

; FILING DATE: 11-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9609576.5

; FILING DATE: 08-MAY-1996

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 484 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; ORIGINAL SOURCE:

; ORGANISM: Mus musculus

US-08-836-620A-14

Query Match 80.6%; Score 2262; DB 2; Length 484;

Best Local Similarity 88.0%; Pred. No. 2e-233;

Matches 426; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

Qy 46 MTFYSPAVMYSIPSNVTNLEGGPGRTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQKS 105

Db 1 MAFYSPAVMYSIPSNVTNLEGGPGRTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQKS 60

Qy 106 PWCEARSLEHTLPVNRRTLKRKYSNRCASPVTPGSKRDAHFCAVCSDYASGYHVGWYS 165

Db 61 PWCEARSLEHTLPVNRRTLKRKYGSGCASPVTPSKRDAHFCAVCSDYASGYHVGWYS 120

Qy 166 CEGCKAFFKRISIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRCG 225

Db 121 CEGCKAFFKRISIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRCG 180

Qy 226 YRLVRQRSDAEOLHCAGAKRSKGHAPVRRELLDALSPEQLVLTLEAEPHVLISRP 285

Db 181 YRIVRQRSDAEOLHCAGAKRSKGHAPVRRELLDALSPEQLVLTLEAEPHVLISRP 240

Qy 286 SAEFTASMMSTLKLADKELVHMISWAKIPGFVELSLDFQVRLLESQWMEVLMGLMW 345

Db 241 SAEFTASMMSTLKLADKELVHMISWAKIPGFVELSLDFQVRLLESQWMEVLMGLMW 300

Qy 346 RSIDHPGKLIFAPDLVLDREDEGKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMIL 405

Db 301 RSIDHPGKLIFAPDLVLDREDEGKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMIL 360

Qy 406 LNSMYPLVATQADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLLMLLSHV 465

Db 361 LNSMYHLATASQAEASSRKLTHLNAVTDALVWVIKSKRISQQSVRLANLLMLLSHV 420

Qy 466 RHASNKGHEHLLSNKCKNNVYVYDILLEMLNAHTLRYKSSISGSGCCSTEDSKSKESQ 525

Db 421 RHISNKGHEHLLSNKCKNNVYVYDILLEMLNAHTLRYKSSISGSGCCSTEDSKSKESQ 480

Qy 526 NPOS 529

Db 481 NLQS 484

RESULT 11

US-09-608-088-6

; Sequence 6, Application US/09608089

; Patent No. 6680368

; GENERAL INFORMATION:

; APPLICANT: Mosselman, Sietse

; APPLICANT: Dijkema, Rein

; TITLE OF INVENTION: No. 6680368e1 Estrogen Receptor

; FILE REFERENCE: 0/96193 US/D1

; CURRENT APPLICATION NUMBER: US/09/608,088

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 08/826,361

; PRIOR FILING DATE: 1997-03-26

; PRIOR APPLICATION NUMBER: EP 96203284.3

; PRIOR FILING DATE: 1996-11-22

; PRIOR APPLICATION NUMBER: EP 96200820.7

; PRIOR FILING DATE: 1996-03-26

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 6

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-608-088-6

Query Match 78.4%; Score 2198; DB 4; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.1e-226;

Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 MNYSPSNVTNLEGGPGRTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEARSL 113

Db 1 MNYSPSNVTNLEGGPGRTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEARSL 60

Qy 114 EHTLPVNRRTLKRKYSNRCASPVTPGSKRDAHFCAVCSDYASGYHVGWYSCGCKAFP 173

Db 61 EHTLPVNRRTLKRKYSNRCASPVTPGSKRDAHFCAVCSDYASGYHVGWYSCGCKAFP 120

Qy 174 KRISIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRCGRLVRRQR 233

Db 121 KRISIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRCGRLVRRQR 180

Qy 234 SADEQLHCAGAKRSKGHAPVRRELLDALSPEQLVLTLEAEPHVLISRPSPAPTEAS 293

Db 181 SADEQLHCAGAKRSKGHAPVRRELLDALSPEQLVLTLEAEPHVLISRPSPAPTEAS 240

Qy 294 MMSLTKLADKELVHMISWAKIPGFVELSLDFQVRLLESQWMEVLMGLMWRSIDHPGK 353

Db 241 MMSLTKLADKELVHMISWAKIPGFVELSLDFQVRLLESQWMEVLMGLMWRSIDHPGK 300

Qy 354 LIAPDLVLDREDEGKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMILNLSMYPL 413

Db 301 LIAPDLVLDREDEGKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMILNLSMYPL 360

Qy 414 VTATQADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLLMLLSHVSHA 468

Db 361 VTATQADSSRKLHLNAVTDALVWVIKSGISSQQSMRLANLLMLLSHVSHA 415

RESULT 12

US-09-608-088-21  
; Sequence 21, Application US/09608088  
; Patent No. 6680369  
; GENERAL INFORMATION:  
; APPLICANT: Mosselman, Sietse  
; APPLICANT: Dijkema, Rein  
; TITLE OF INVENTION: No. 6680368e1 Estrogen Receptor  
; FILE REFERENCE: O/96193 US/D1  
; CURRENT APPLICATION NUMBER: US/09/608,088  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 08/826,361  
; PRIOR FILING DATE: 1997-03-26  
; PRIOR APPLICATION NUMBER: EP 96203284.3  
; PRIOR FILING DATE: 1996-11-22  
; PRIOR APPLICATION NUMBER: EP 96200820.7  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 21  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-608-088-21

Query Match 78.4%; Score 2198; DB 4; Length 418;  
Best Local Similarity 100.0%; Pred. No. 1.1e-226;  
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 MNYSPSNVTNLEGGPGROTTSPNVLPWTPGHLSPVLRQSHLYAEQKSPWCEARSL 113  
DB 1 MNYSPSNVTNLEGGPGROTTSPNVLPWTPGHLSPVLRQSHLYAEQKSPWCEARSL 60

QY 114 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSDYASGHHYGVMSCEGCKAFF 173  
DB 61 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSDYASGHHYGVMSCEGCKAFF 120

QY 174 KRSIQGHNDYICPATNCTIDKRRKSCQACRLKCYEVMKCGSRRCGRLVRROR 233  
DB 121 KRSIQGHNDYICPATNCTIDKRRKSCQACRLKCYEVMKCGSRRCGRLVRROR 180

QY 234 SADEQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLEAPPHVLSRPSAPTEAS 293  
DB 181 SADEQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLEAPPHVLSRPSAPTEAS 240

QY 294 MMMSLTKLADKELVHMISWAKKIPGFVELSLPQVRLLESCHWVEVLMGLMWSRIDHPCK 353  
DB 241 MMMSLTKLADKELVHMISWAKKIPGFVELSLPQVRLLESCHWVEVLMGLMWSRIDHPCK 300

QY 354 LIFAPDLVLRDRGKCVGEILEIFDMLLATTSPRELKLQHKYLCVKAMILLNSSMYPL 413  
DB 301 LIFAPDLVLRDRGKCVGEILEIFDMLLATTSPRELKLQHKYLCVKAMILLNSSMYPL 360

QY 414 VTATQDADSSRLKLAHLINAVTDALVWVIKSGISSQQQSRMLANLMLLSHVRHA 468  
DB 361 VTATQDADSSRLKLAHLINAVTDALVWVIKSGISSQQQSRMLANLMLLSHVRHA 415

RESULT 13  
US-08-836-620A-15  
; Sequence 15, Application US/08836620A  
; Patent No. 5958710  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,620A  
; FILING DATE:

PRIOR APPLICATION DATA: PCT/EP96/03933  
; APPLICATION NUMBER: GB 9518272.1  
; FILING DATE: 08-SEP-1995  
; FILING DATE: 08-SEP-1995  
; PRIOR APPLICATION NUMBER: GB 9605550.4  
; FILING DATE: 15-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9607532.0  
; FILING DATE: 11-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9609576.5  
; FILING DATE: 08-MAY-1996  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORGANISM: Homo sapiens  
US-08-836-620A-15

Query Match 71.9%; Score 2017; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 2.5e-207;  
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 LSPLVVRHQLSHLYAEQKSPWCEARSLHTLPVNRRLTKRKVSGNRCASPVTPGSKRD 145  
DB 2 LSPLVVRHQLSHLYAEQKSPWCEARSLHTLPVNRRLTKRKVSGNRCASPVTPGSKRD 61

QY 146 AHFCVCSDYASGHHYGVMSCEGCKAFFKRSIQGHNDYICPATNCTIDKRRKSCQACR 205  
DB 62 AHFCVCSDYASGHHYGVMSCEGCKAFFKRSIQGHNDYICPATNCTIDKRRKSCQACR 121

QY 206 LRKCYEVMKCGSRRCGRLVRRORSADEQLHCAGKAKSGGHPRVRELLLDALSP 265  
DB 122 LRKCYEVMKCGSRRCGRLVRRORSADEQLHCAGKAKSGGHPRVRELLLDALSP 181

QY 266 BOLVLTLEAPPHVLSRPSAPTEASMMSLTKLADKELVHMISWAKKIPGFVELSLF 325  
DB 182 BOLVLTLEAPPHVLSRPSAPTEASMMSLTKLADKELVHMISWAKKIPGFVELSLF 241

QY 326 DOVRLLESCHWVEVLMGLMWSRIDHPGKLIIFAPDLVLRDRGKCVGEILEIFDMLLATT 385  
DB 242 DOVRLLESCHWVEVLMGLMWSRIDHPGKLIIFAPDLVLRDRGKCVGEILEIFDMLLATT 301

QY 386 RFRELKLQHKYLCVKAMILLNSSMYPLVTATQDADSSRLKLAHLINAVTDALVWVIKSG 445  
DB 302 RFRELKLQHKYLCVKAMILLNSSMYPLVTATQDADSSRLKLAHLINAVTDALVWVIKSG 361

QY 446 ISSQQQSRMLANLMLLSHVRHA 468  
DB 362 ISSQQQSRMLANLMLLSHVRHA 384

RESULT 14  
US-08-764-870-12  
; Sequence 12, Application US/08764870  
; Patent No. 6236946  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S  
; APPLICANT: Baxter, John D  
; APPLICANT: Fletcher, Robert J  
; APPLICANT: Wagner, Richard L  
; APPLICANT: Kushner, Peter J  
; APPLICANT: Aprelitti, James W  
; APPLICANT: West, Brian  
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
; TITLE OF INVENTION: Binding Domains  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward

US-09-608-088-21  
; Sequence 21, Application US/09608088  
; Patent No. 6680369  
; GENERAL INFORMATION:  
; APPLICANT: Mosselman, Sietse  
; APPLICANT: Dijkema, Rein  
; TITLE OF INVENTION: No. 6680368e1 Estrogen Receptor  
; FILE REFERENCE: O/96193 US/D1  
; CURRENT APPLICATION NUMBER: US/09/608,088  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 08/826,361  
; PRIOR FILING DATE: 1997-03-26  
; PRIOR APPLICATION NUMBER: EP 96203284.3  
; PRIOR FILING DATE: 1996-11-22  
; PRIOR APPLICATION NUMBER: EP 96200820.7  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 21  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-608-088-21

Query Match 78.4%; Score 2198; DB 4; Length 418;  
Best Local Similarity 100.0%; Pred. No. 1.1e-226;  
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 MNYSPSNVTNLEGGPGROTTSPNVLPWTPGHLSPVLRQSHLYAEQKSPWCEARSL 113  
DB 1 MNYSPSNVTNLEGGPGROTTSPNVLPWTPGHLSPVLRQSHLYAEQKSPWCEARSL 60

QY 114 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSDYASGHHYGVMSCEGCKAFF 173  
DB 61 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSDYASGHHYGVMSCEGCKAFF 120

QY 174 KRSIQGHNDYICPATNCTIDKRRKSCQACRLKCYEVMKCGSRRCGRLVRROR 233  
DB 121 KRSIQGHNDYICPATNCTIDKRRKSCQACRLKCYEVMKCGSRRCGRLVRROR 180

QY 234 SADEQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLEAPPHVLSRPSAPTEAS 293  
DB 181 SADEQLHCAGKAKSGGHPRVRELLLDALSPQLVLTLEAPPHVLSRPSAPTEAS 240

QY 294 MMMSLTKLADKELVHMISWAKKIPGFVELSLPQVRLLESCHWVEVLMGLMWSRIDHPCK 353  
DB 241 MMMSLTKLADKELVHMISWAKKIPGFVELSLPQVRLLESCHWVEVLMGLMWSRIDHPCK 300

QY 354 LIFAPDLVLRDRGKCVGEILEIFDMLLATTSPRELKLQHKYLCVKAMILLNSSMYPL 413  
DB 301 LIFAPDLVLRDRGKCVGEILEIFDMLLATTSPRELKLQHKYLCVKAMILLNSSMYPL 360

QY 414 VTATQDADSSRLKLAHLINAVTDALVWVIKSGISSQQQSRMLANLMLLSHVRHA 468  
DB 361 VTATQDADSSRLKLAHLINAVTDALVWVIKSGISSQQQSRMLANLMLLSHVRHA 415

RESULT 13  
US-08-836-620A-15  
; Sequence 15, Application US/08836620A  
; Patent No. 5958710  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,620A  
; FILING DATE:

STREET: Five Palo Alto Square, 3000 El Camino Real  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,870  
FILING DATE: 13-DEC-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,540  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,543  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,606  
FILING DATE: 14-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: UCAL-246/0105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)843-5000  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-764-870-12

Query Match 44.0%; Score 1233.5; DB 3; Length 595;  
Best Local Similarity 48.4%; Pred. No. 5.2e-123;  
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;  
  
QY 5 NSPSSLSNPSYNCSSQSLPLEH--GSIIYIPSS--YVDSHHEYPAMTFYSPAVMYNYSIPS 60  
DB 21 NELEPLNRP-----QKIPLERPLGEVLDSSKPAVNYPEGAAYEFNAANAQAQVYG 74  
  
QY 61 NVTNLEGGPGRQ-----TTSNPNVLPPTGHLSP-LVVRQLSHLYAE 101  
DB 75 Q-TGLPYGPGSEAAAFSGNLGPGFPPLNSVSPSLMLLHPPLQSPFLQHGQVPPYLE 133  
  
QY 102 PQKSPWC--EARSLEHTLPVNRRETLKRVKSGNRCASPVTPGP-----SKDAHFCAVCS 154  
DB 134 NEPSGYTVREAGPPAFYRP-----NSDNRROGQRELRSTNDKGSMAESAKETRYCAVCND 190  
  
QY 155 YASGYHYGVNCSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGM 214  
DB 191 YASGYHYGVNCSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGM 250  
  
QY 215 VKGSRRCRCYRLVRQRSADEQLHCAGKAKKSGGHA PRV-----EL 258  
DB 251 MKGGRKDRGGRMLKHKRQDD-----GEGRGVGSAGDMRAANLWPSPLMKRSKNS 305  
  
QY 259 LLDALSPQVLTLLEAPPPHVLISR--PSAPFTEASMMMSLTKLADKELVHMSWAKKI 316  
DB 306 LALSADQWYSAILDAPPP--ILYSEYDPTFPFSEASMMGLTTLADRELVHMLNWAQV 364  
  
QY 317 PGFVELSLFDQVRLLESCEMVLMMWRSIDHFGKLIIPAPDLVDRDRCKVEGILEI 376  
DB 365 PGFVDLTLDQVHLECAWLBIIMGLVWRSMHFGKLLFAPNLLDRNQGCKVEGMEI 424  
  
QY 377 FDMILLATTSRRELKLOHKEYLVKAMILLNMSMYPLVAT--QDADSSRLKHLNNAVTD 435  
DB 425 FDMILLATTSRRELKLOHKEYLVKAMILLNMSMYPLVAT--QDADSSRLKHLNNAVTD 484

QY 436 ALVWVIAKSGISSQOOSMELANILMLLSHVTHASNKGMEHLNMMKCNVVPVYDILLEML 495  
DB 485 TLHLAKAGLTIQOQHQLAQLLLSHIRMSNKGMEHLYSMKCNVVPVYDILLEML 544  
  
QY 496 NAHVL 500  
DB 545 DAHRL 549  
  
RESULT 15  
US-08-980-115-12  
Sequence 12, Application US/08980115  
Patent No. 6266622  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Thomas S.  
APPLICANT: Baxter, John D.  
APPLICANT: Fletcher, Robert J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Apriletti, James W.  
APPLICANT: West, Brian L.  
APPLICANT: Shiau, Andrew K.  
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
FILE REFERENCE: UCAL-246/0205  
CURRENT APPLICATION NUMBER: US/08/980,115  
CURRENT FILING DATE: 1997-11-26  
EARLIER APPLICATION NUMBER: 08/764,870  
EARLIER FILING DATE: 1996-12-13  
EARLIER APPLICATION NUMBER: 60/008,606  
EARLIER FILING DATE: 1995-12-14  
EARLIER APPLICATION NUMBER: 60/008,543  
EARLIER FILING DATE: 1995-12-13  
EARLIER APPLICATION NUMBER: 60/008,540  
EARLIER FILING DATE: 1995-12-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 12  
LENGTH: 595  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (287)...(549)  
OTHER INFORMATION: minimal ligand binding domain  
US-08-980-115-12

Query Match 44.0%; Score 1233.5; DB 3; Length 595;  
Best Local Similarity 48.4%; Pred. No. 5.2e-123;  
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;  
  
QY 5 NSPSSLSNPSYNCSSQSLPLEH--GSIIYIPSS--YVDSHHEYPAMTFYSPAVMYNYSIPS 60  
DB 21 NELEPLNRP-----QKIPLERPLGEVLDSSKPAVNYPEGAAYEFNAANAQAQVYG 74  
  
QY 61 NVTNLEGGPGRQ-----TTSNPNVLPPTGHLSP-LVVRQLSHLYAE 101  
DB 75 Q-TGLPYGPGSEAAAFSGNLGPGFPPLNSVSPSLMLLHPPLQSPFLQHGQVPPYLE 133  
  
QY 102 PQKSPWC--EARSLEHTLPVNRRETLKRVKSGNRCASPVTPGP-----SKDAHFCAVCS 154  
DB 134 NEPSGYTVREAGPPAFYRP-----NSDNRROGQRELRSTNDKGSMAESAKETRYCAVCND 190  
  
QY 155 YASGYHYGVNCSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGM 214  
DB 191 YASGYHYGVNCSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVGM 250  
  
QY 215 VKGSRRCRCYRLVRQRSADEQLHCAGKAKKSGGHA PRV-----EL 258  
DB 251 MKGGRKDRGGRMLKHKRQDD-----GEGRGVGSAGDMRAANLWPSPLMKRSKNS 305  
  
QY 259 LLDALSPQVLTLLEAPPPHVLISR--PSAPFTEASMMMSLTKLADKELVHMSWAKKI 316



Db	306	LALSLTADQWVSALLDAEPP-ILYSEYDTPFPSEASMGLLTNTLADRELVEHINWAKRV	364
Qy	317	PGFVELSLFDQVRLLESQWNEVLAMGLMFRSIDIHPGKLIAPADVLDRDEGKCVGILEI	376
Db	365	PGFVDTLTHDQVHLLCAMLLEILMIGLVFRSMEHPGKLEFAPNLLDRNQKCVGNVEI	424
Qy	377	FDMLATTSSRFELKQHKYLCVKAMILLNSSNYPLVATAT-ODADSSRKLAHLNAVED	435
Db	425	FDMLLATSSRFMMNLQGEFVCLKSHILLANSGVYTFPLSSTLSLEBKDHHRVLDKITD	484
Qy	436	ALVWVIKSGISSQQQSMRLANLLMLSHVFRHASNKGMEHLNKKCNVVPVYDILLEML	495
Db	485	TLJHLMAKAGLTLQQQHORIQAQLLLILSHIRHNSNKGMEHLYSMKCNVVPVYDILLEML	544
Qy	496	NAEVL 500	
Db	545	DAHRL 549	

Search completed: June 20, 2004, 10:39:47  
Job time : 25 secs